Fungal Planet description sheets: 785–867

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citriodora. **Brazil**, *Calonectria hemileiae* on pustules of *Hemileia vastatrix*formed on leaves of *Coffea arabica*, *Calvatia caatinguensis* on soil, *Cercospora solani-betacei* on *Solanum betaceum*, *Clathrus natalensis* on soil, *Diaporthe poincianellae* on *Poincianella pyramidalis*, *Geastrum piquiriunense* on soil, *Geosmithia carolliae* on wing of *Carollia perspicillata*, *Henningsia resupinata* on wood, *Penicillium guaibinense* from soil, *Periconia caespitosa* from leaf litter, *Pseudocercospora styracina* on *Styrax*sp., *Simplicillium filiforme* as endophyte from *Citrullus lanatus*, *Thozetella pindobacuensis* on leaf litter, *Xenosonderhenia coussapoae* on *Coussapoa floccosa.* **Canary Islands (Spain)**, *Orbilia amarilla* on *Euphorbia canariensis.* **Cape Verde Islands**, *Xylodon jacobaeus* on *Eucalyptus camaldulensis.* **Chile**, *Colletotrichum arboricola* on *Fuchsia magellanica.* **Costa Rica**, *Lasiosphaeria miniovina* on tree branch. **Ecuador**, *Ganoderma chocoense* on tree trunk. **France**, *Neofitzroyomyces nerii* (incl. *Neofitzroyomyces* gen. nov.) on *Nerium oleander.* **Ghana**, *Castanediella tereticornis* on *Eucalyptus tereticornis*, *Falcocladium africanum* on *Eucalyptus brassiana*, *Rachicladosporium corymbiae* on *Corymbia citriodora.* **Hungary**, *Entoloma silvae-frondosae* in *Carpinus betulus-Pinus sylvestris* mixed forest. **Iran**, *Pseudopyricularia persiana* on *Cyperus* sp.**Italy**, *Inocybe roseascens* on soil in mixed forest. **Laos**, *Ophiocordyceps houaynhangensis* on *Coleoptera* larva. **Malaysia**, *Monilochaetes melastomae* on *Melastoma* sp. **Mexico**, *Absidia terrestris* from soil. **Netherlands**, *Acaulium pannemaniae*, *Conioscypha boutwelliae*, *Fusicolla septimanifiniscientiae*, *Gibellulopsis simonii*, *Lasionectria hilhorstii*, *Lectera nordwiniana, Leptodiscella rintelii, Parasarocladium debruynii* and *Sarocladium dejongiae* (incl. *Sarocladiaceae* fam. nov.) from soil. **New Zealand**, *Gnomoniopsis rosae* on *Rosa* sp. and *Neodevriesia metrosideri* on *Metrosideros* sp. **Puerto Rico**, *Neodevriesia coccolobae* on *Coccoloba uvifera*, *Neodevriesia tabebuiae* and *Alfaria tabebuiae* on *Tabebuia chrysantha*. **Russia**, *Amanita paludosa* on bogged soil in mixed deciduous forest, *Entoloma tiliae* in forest of *Tilia* × *europaea*, *Kwoniella endophytica* on *Pyrus communis.* **South Africa**, *Coniella diospyri* on *Diospyros mespiliformis, Neomelanconiella combreti* (incl. *Neomelanconiellaceae* fam. nov. and *Neomelanconiella* gen. nov.) on *Combretum* sp., *Polyphialoseptoria natalensis* on unidentified plant host, *Pseudorobillarda bolusanthi* on *Bolusanthus speciosus*, *Thelonectria pelargonii* on *Pelargonium* sp. **Spain**, *Vermiculariopsiella lauracearum* and *Anungitopsis lauri* on *Laurus novocanariensis*, *Geosmithia xerotolerans* from a darkened wall of a house, *Pseudopenidiella gallaica* on leaf litter. **Thailand**, *Corynespora thailandica* on wood, *Lareunionomyces loeiensis* on leaf litter, *Neocochlearomyces chromolaenae* (incl. *Neocochlearomyces* gen. nov.) on *Chromolaena odorata, Neomyrmecridium septatum* (incl. *Neomyrmecridium* gen. nov.), *Pararamichloridium caricicola* on *Carex* sp., *Xenodactylaria thailandica* (incl. *Xenodactylariaceae* fam. nov. and *Xenodactylaria* gen. nov.), *Neomyrmecridium asiaticum* and *Cymostachys thailandica* from unidentified vine. **USA**, *Carolinigaster bonitoi*(incl. *Carolinigaster* gen. nov.) from soil, *Penicillium fortuitum* from house dust, *Phaeotheca shathenatiana*(incl. *Phaeothecaceae* fam. nov.) from twig and cone litter, *Pythium wohlseniorum* from stream water, *Superstratomyces tardicrescens* from human eye, *Talaromyces*

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Keywords: ITS nrDNA barcodes | LSU | new taxa | systematics

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Abstract (cont.)

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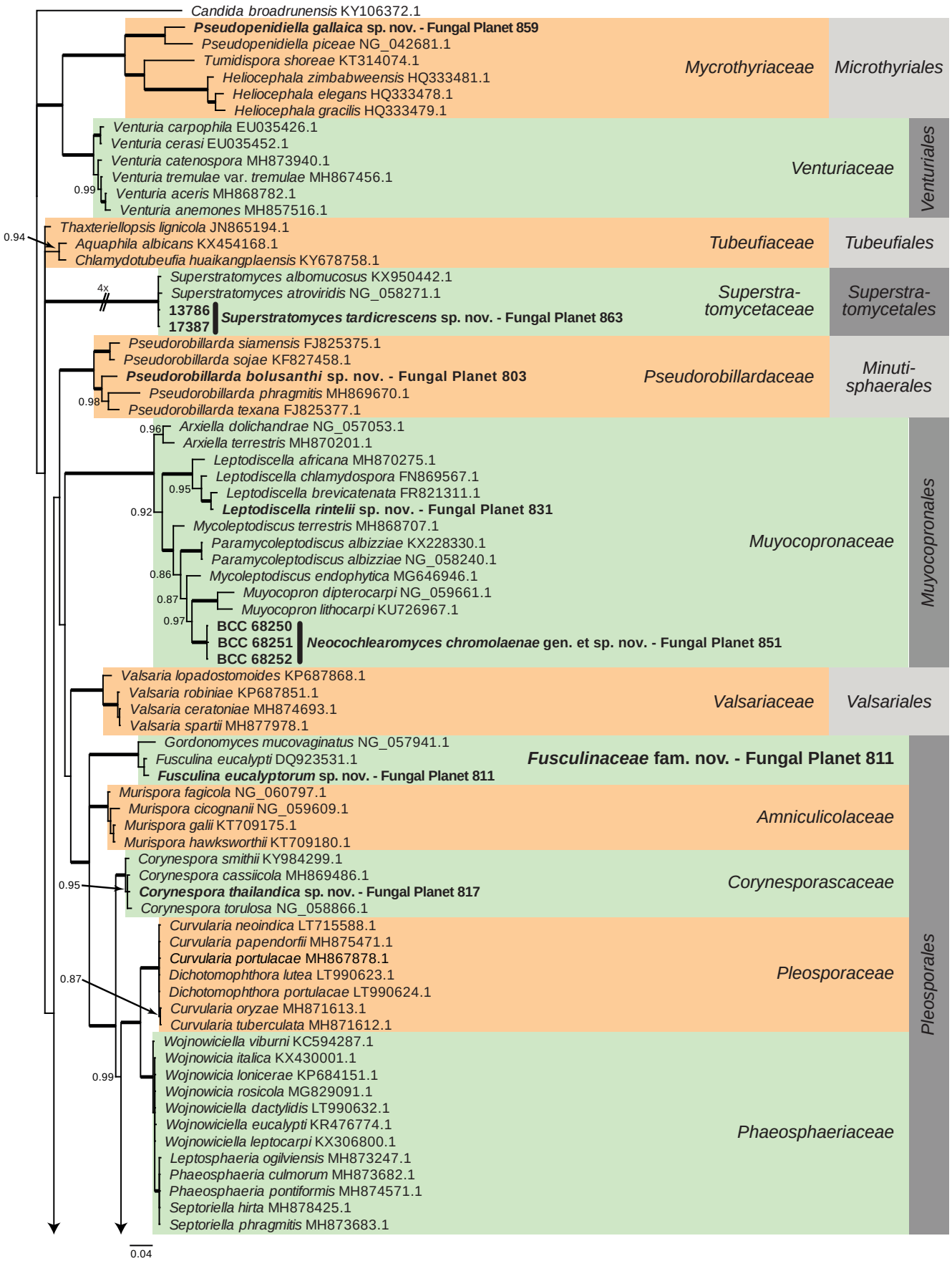
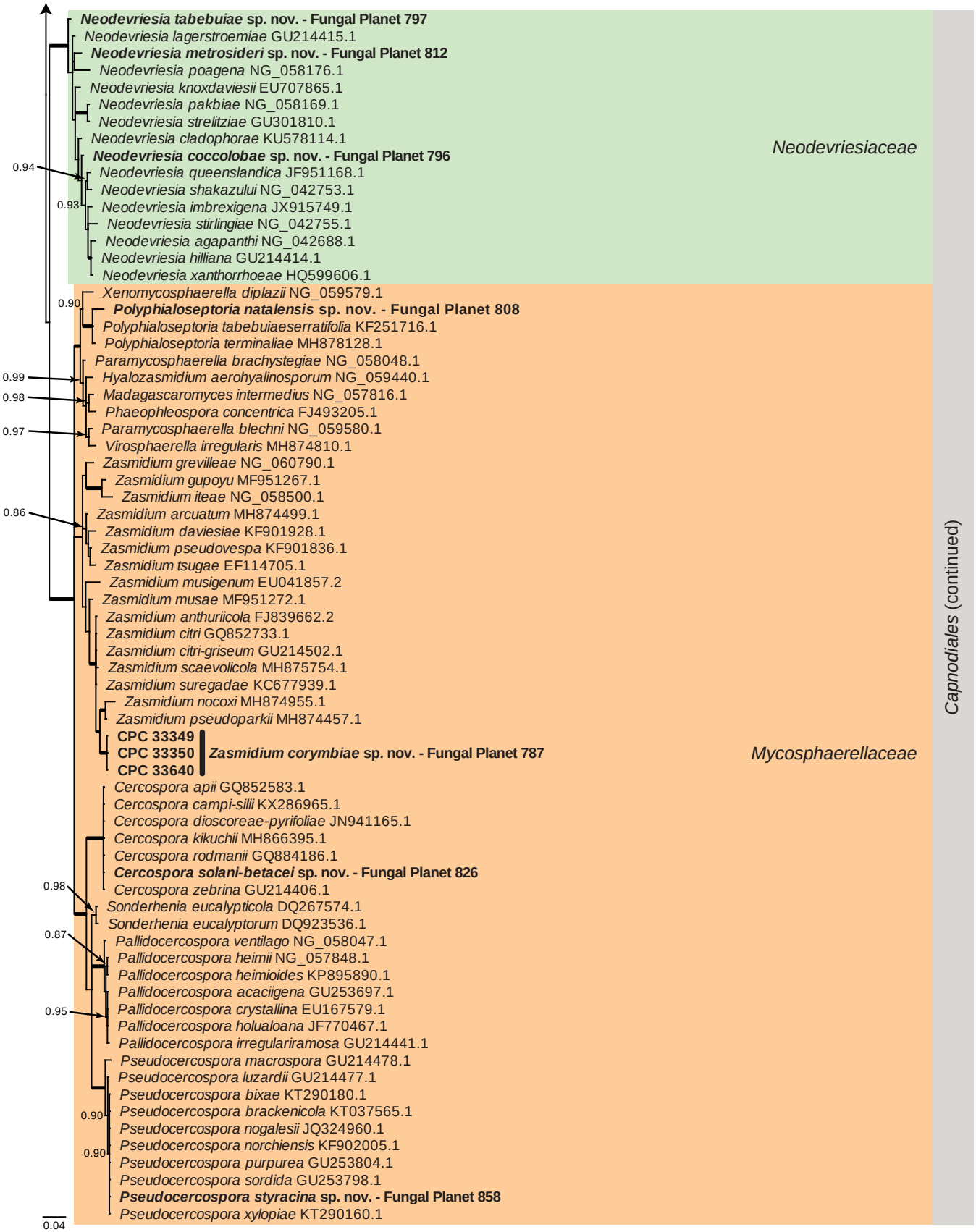


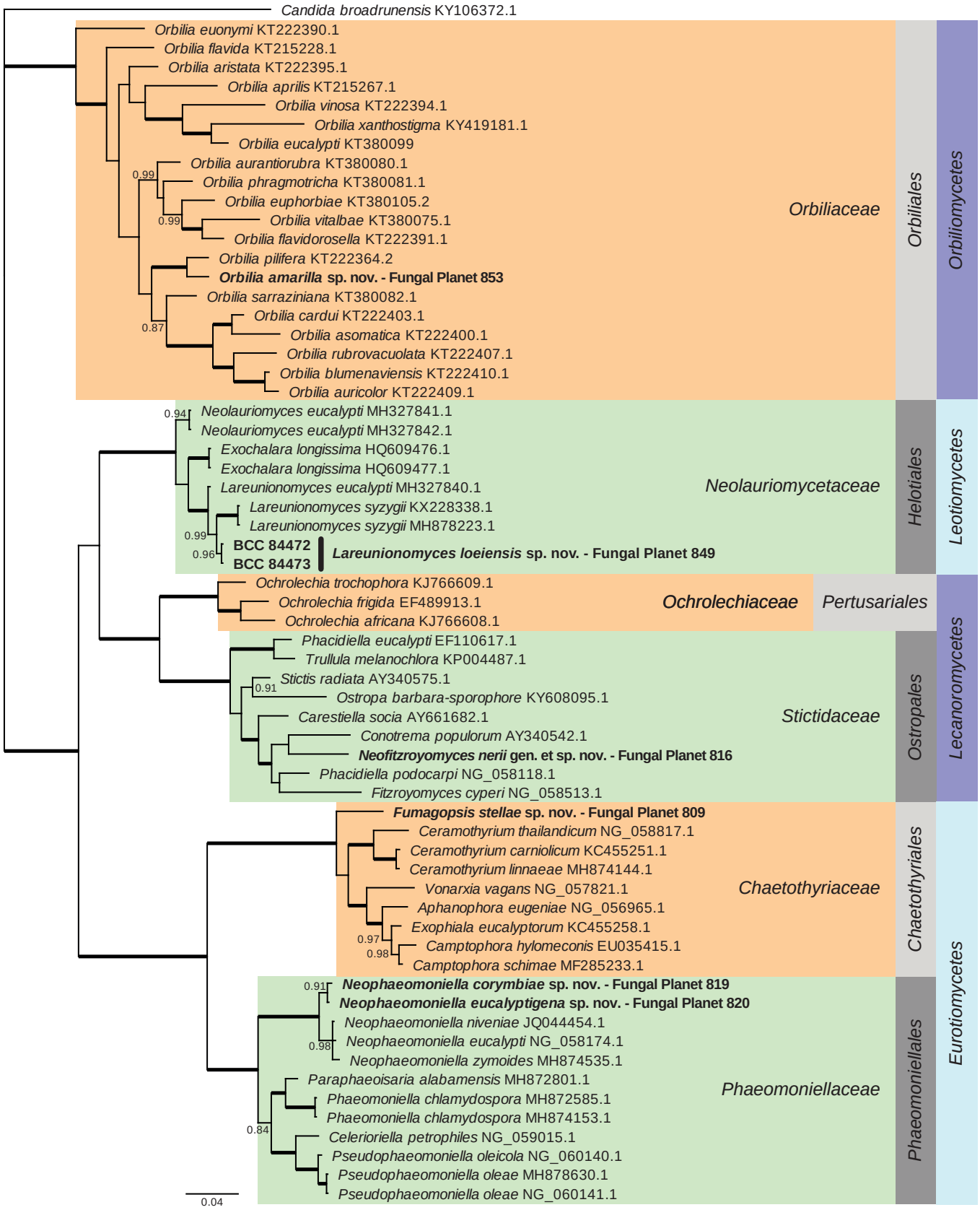
Overview *Dothideomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 2 478 trees resulting from a Bayesian analysis of the LSU sequence alignment (206 taxa including outgroup; 801 aligned positions; 464 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).

Overview *Dothideomycetes* phylogeny (cont.) – part 2

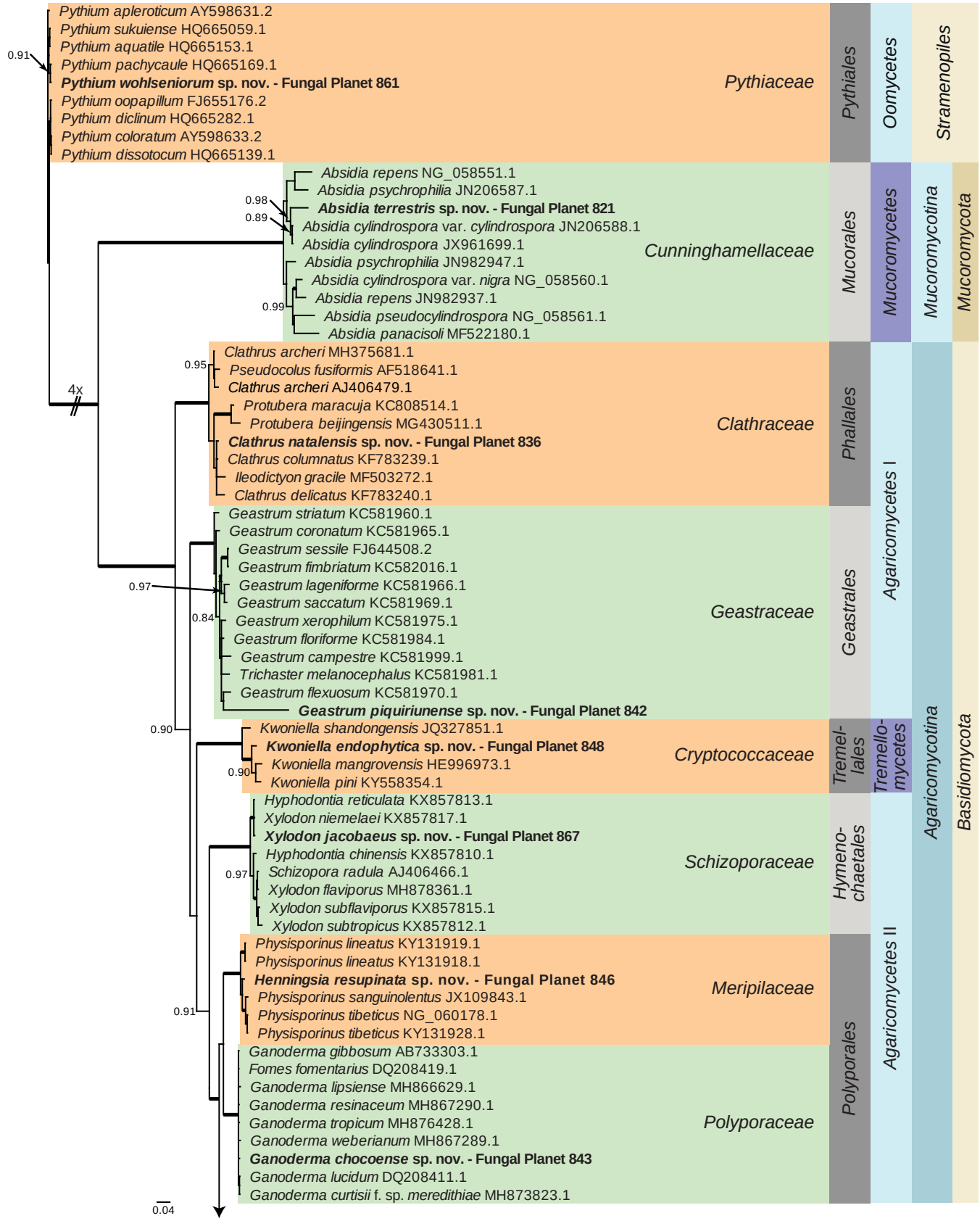


Overview *Dothideomycetes* phylogeny (cont.) – part 3



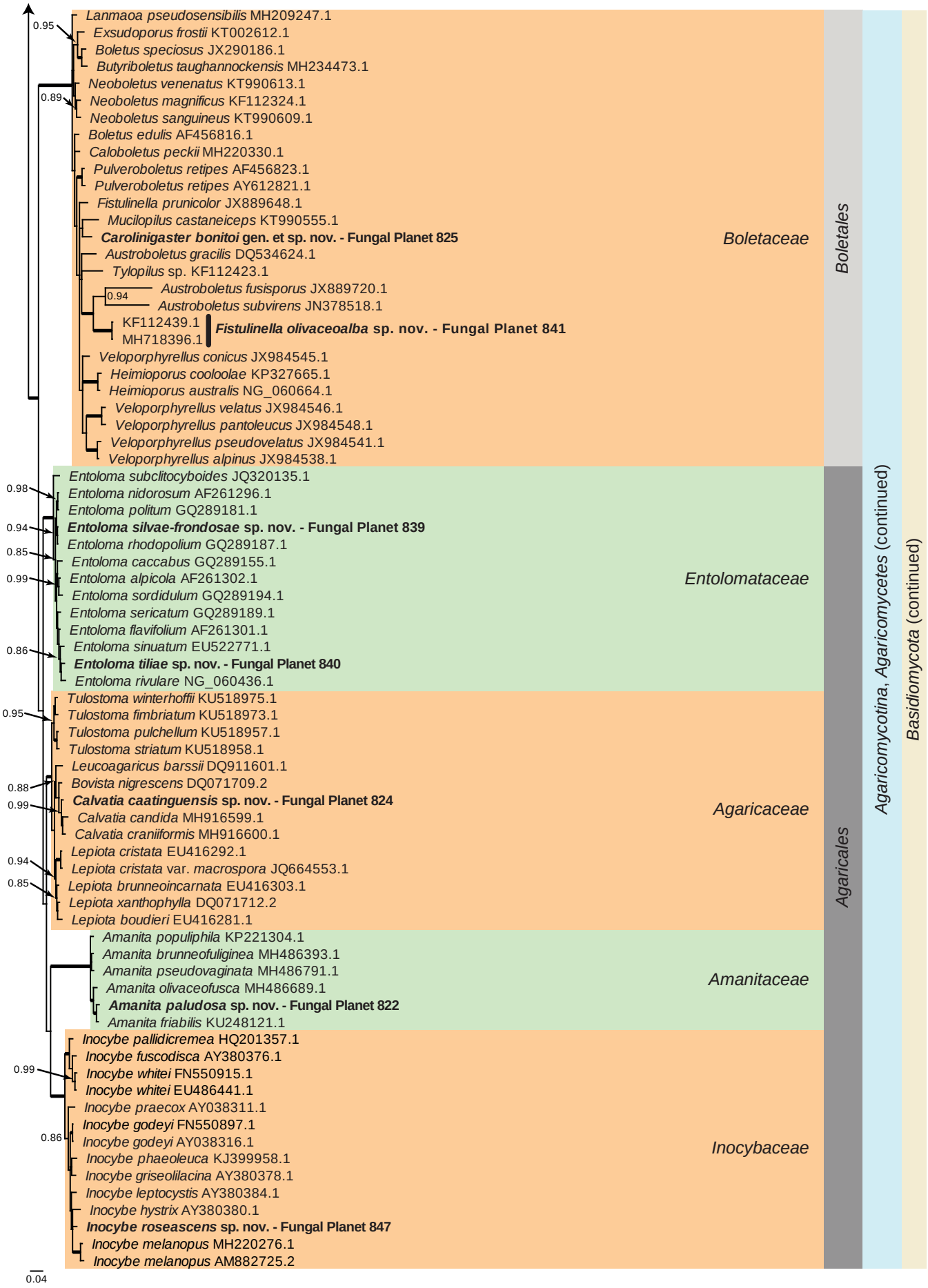
Overview *Orbiliomycetes*, *Leotiomycetes*, *Lecanoromycetes* and *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 12452 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 taxa including outgroup; 829 aligned positions; 360 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).

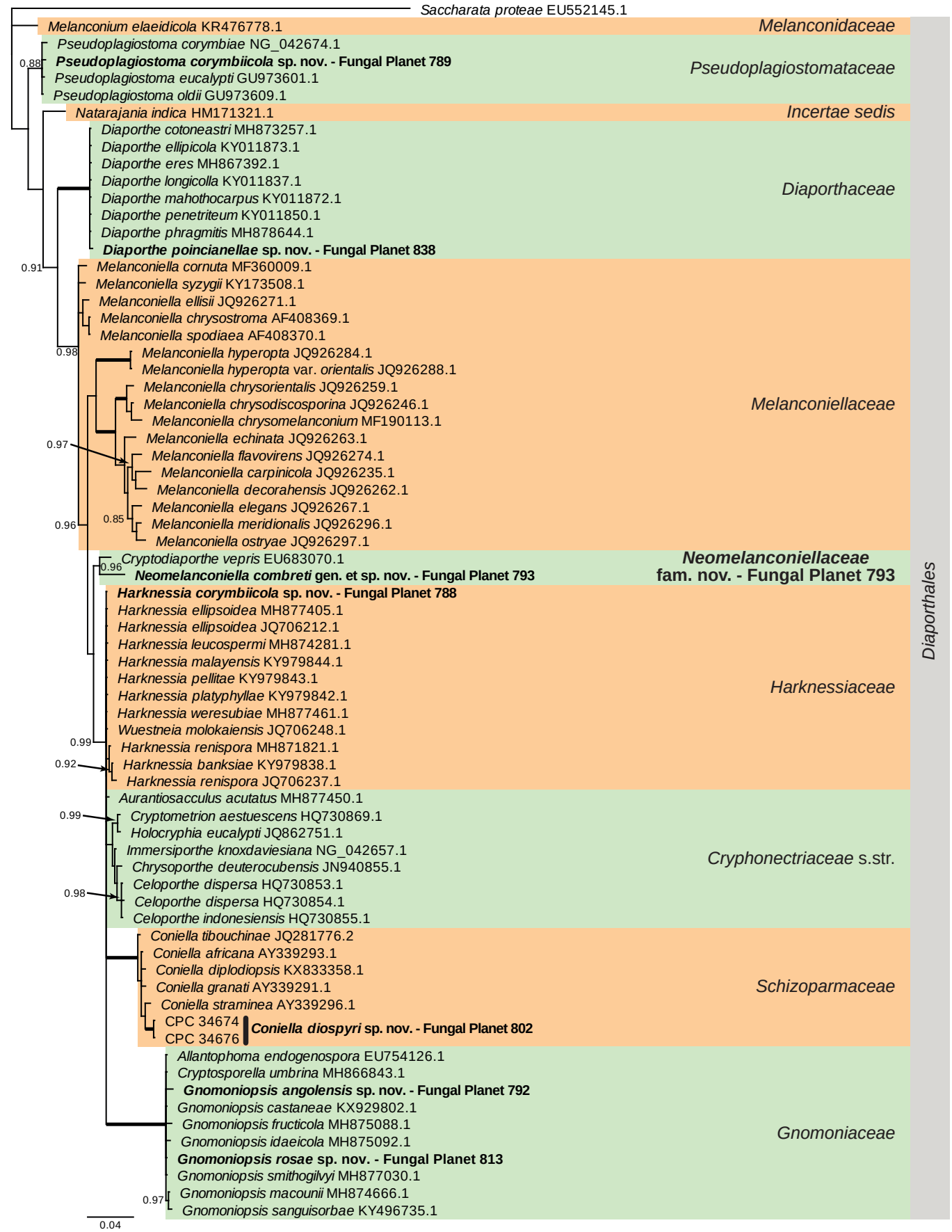


Overview *Stramenopiles*, *Mucoromycota* and *Basidiomycota* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 113 852 trees resulting from a Bayesian analysis of the LSU sequence alignment (141 taxa including outgroup; 980 aligned positions; 654 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders, classes, subdivisions and phyla are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to the *Stramenopiles* clade and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).

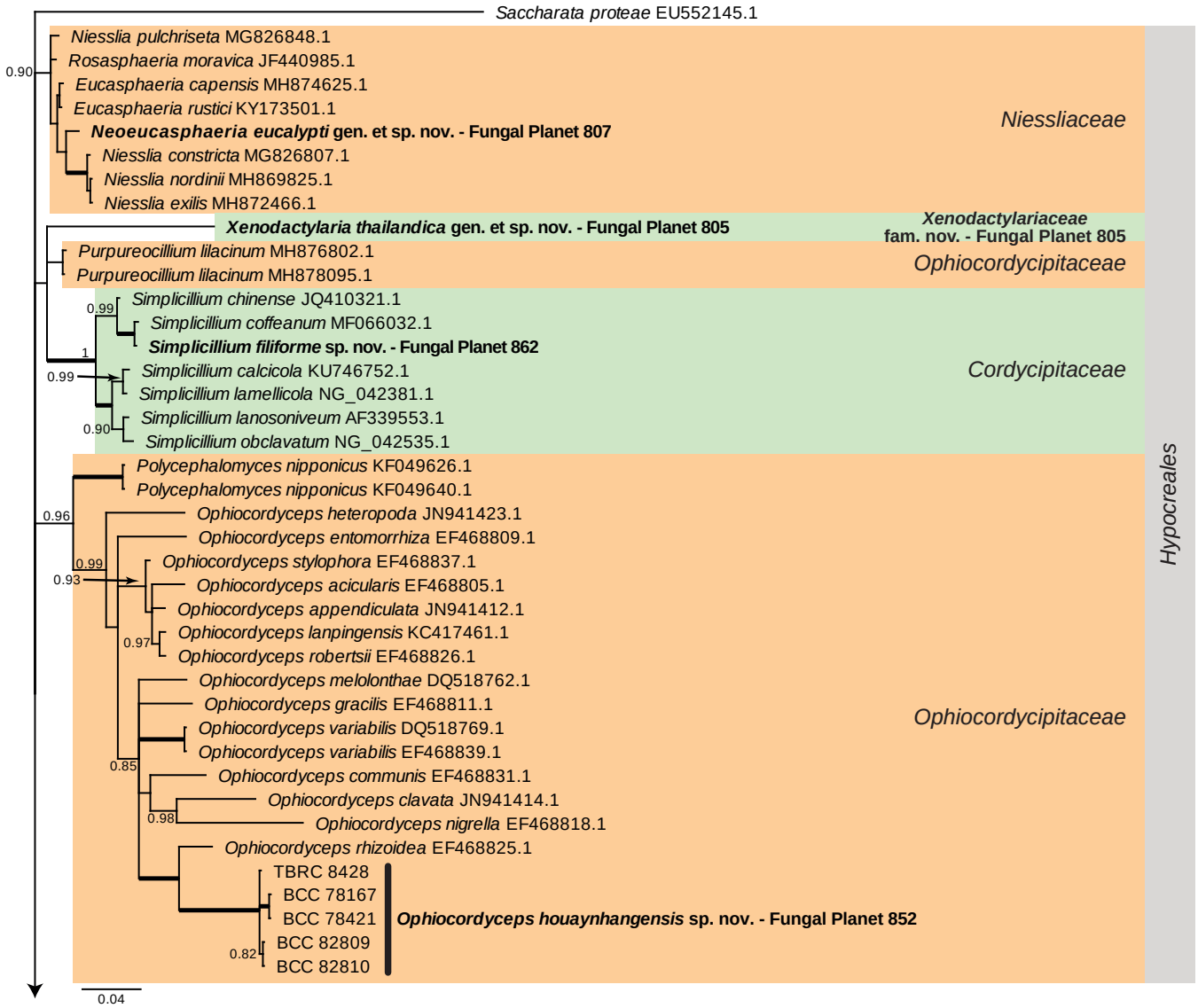


Overview *Stramenopiles*, *Mucoromycota* and *Basidiomycota* phylogeny (cont.) – part 2



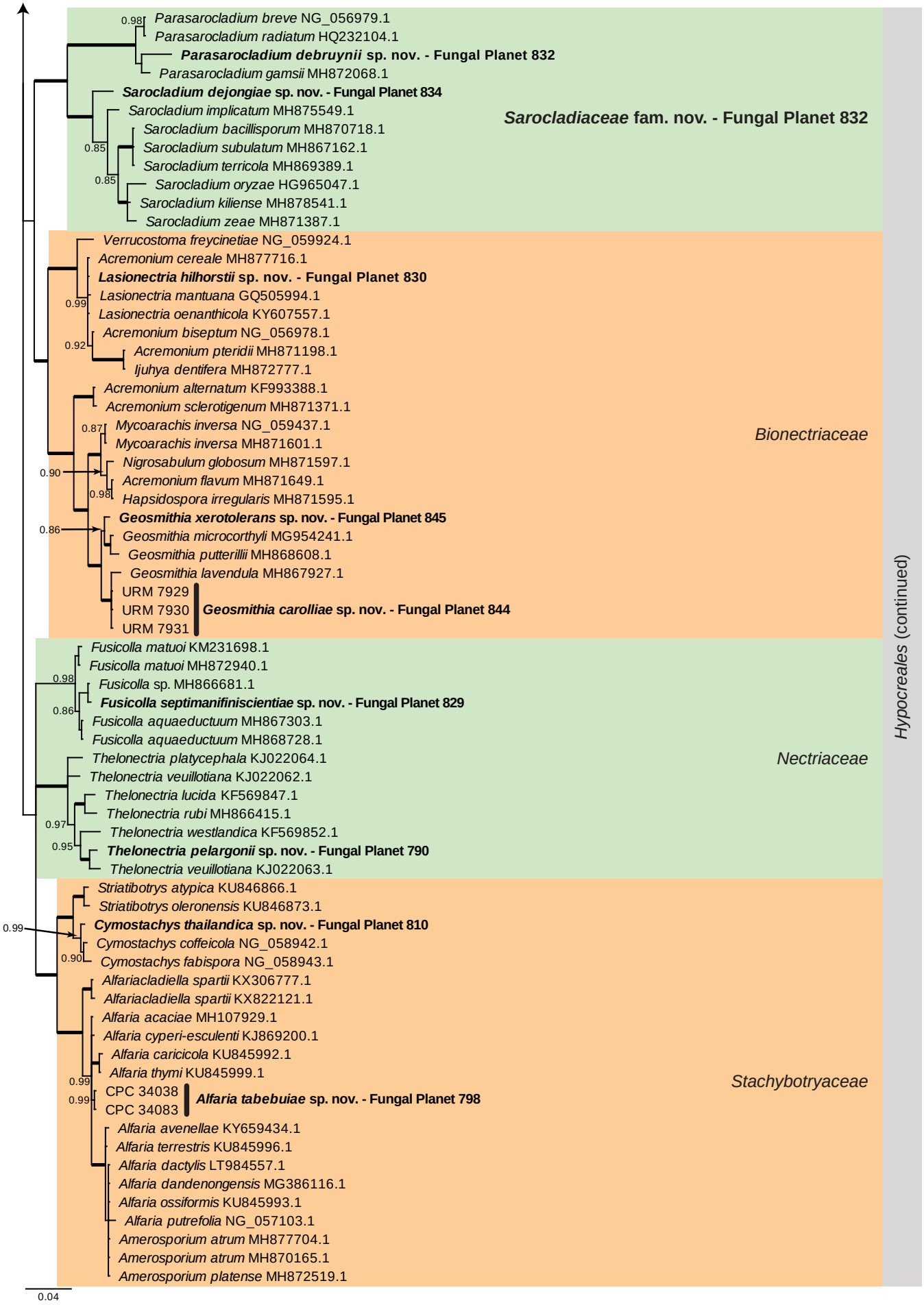
Overview *Diaporthales* (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 1 052 trees resulting from a Bayesian analysis of the LSU sequence alignment (71 taxa including outgroup; 768 aligned positions; 176 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).

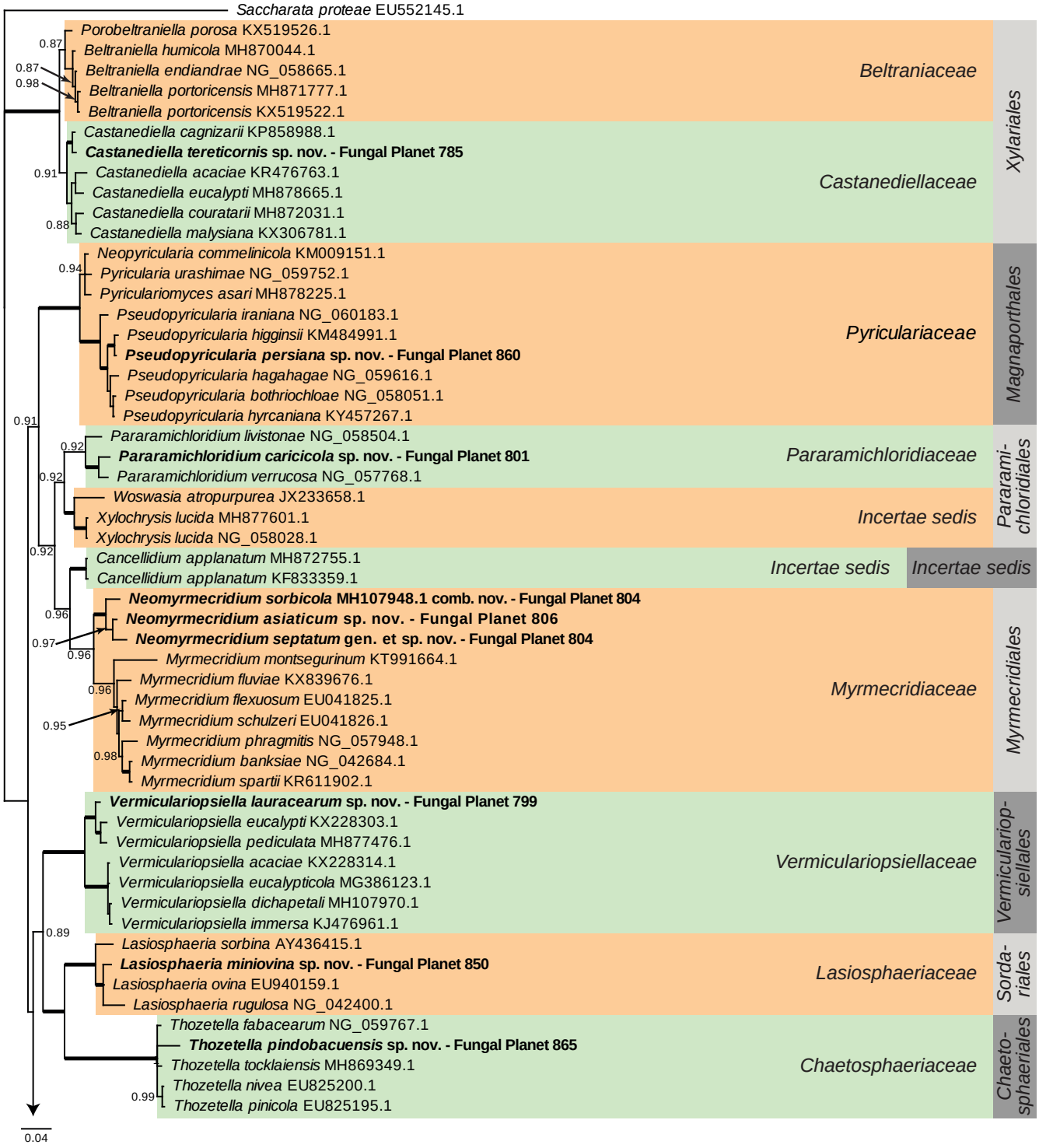


Overview *Hypocreales* (*Sordariomycetes*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 3078 trees resulting from a Bayesian analysis of the LSU sequence alignment (110 taxa including outgroup; 820 aligned positions; 339 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).

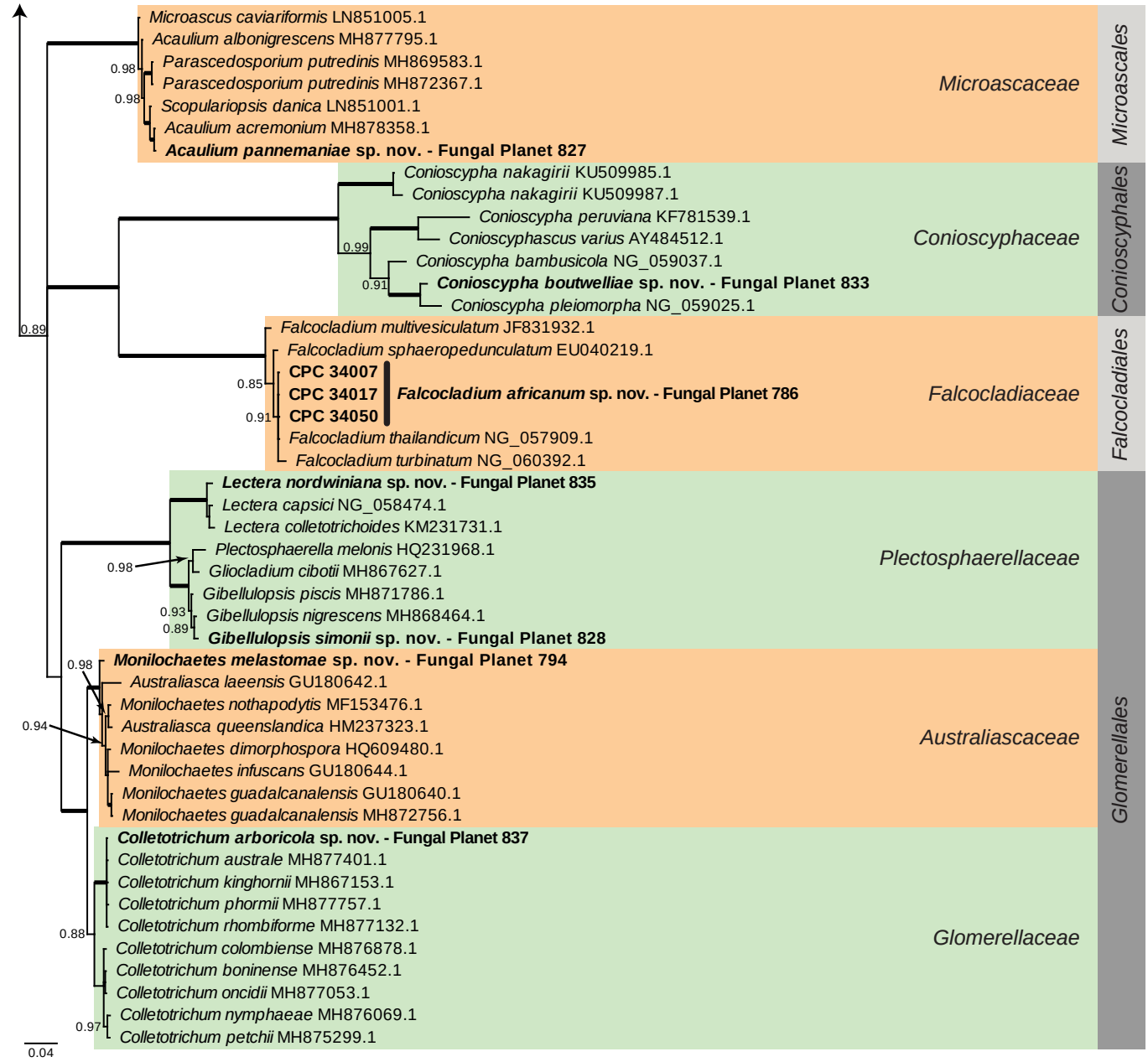


Overview *Hypocreales* (*Sordariomycetes*) phylogeny (cont.) – part 2



Overview other orders (*Sordariomycetes*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (102 taxa including outgroup; 782 aligned positions; 396 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S23436).



Overview other orders (*Sordariomycetes*) phylogeny (cont.) – part 2


Castanediella tereticornis
& Falcocladium africanum

Fungal Planet 785 & 786 – 14 December 2018

Castanediella tereticornis Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus tereticornis*, the host species from which this fungus was isolated.

Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of olivaceous, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, pale brown, smooth, subcylindrical, unbranched, 0–2-septate, 5–30 × 2–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 5–20 × 2–3 µm, apex at times slightly swollen, with several denticulate loci, 0.5–2 × 1–1.5 µm, unthickened, not darkened. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, 1-septate, subcylindrical, straight, inner plane flat, outer plane convex, apex acutely rounded, tapering to flat inner plane, base truncate, 0.5–1 µm diam, tapering toward inner flat plane, (16–)17–20(–22) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface isabelline with diffuse red pigment, reverse dark brick; on PDA surface and reverse isabelline; on OA surface sepia.

Typus. Ghana, on leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 21 June 2010, *M.J. Wingfield*, HPC 2175 (holotype CBS H-23765, culture ex-type CPC 34027 = CBS 145068, ITS and LSU sequences GenBank MK047417.1 and MK047468.1, MycoBank MB828165).

Notes — *Castanediella* was introduced for idriella-like fungi, distinguished by having branched conidiophores giving rise to straight or slightly curved conidia (Crous et al. 2015b, 2017b, Hernández-Restrepo et al. 2016, 2017). *Castanediella tereticornis* is phylogenetically distinct from the 12 species presently accepted in the genus, all of which are known from DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Castanediella cagnizarii* (GenBank NR_156294.1; Identities = 543/555 (98 %), 6 gaps (1 %)), *Castanediella hyalopenicillata* (GenBank NR_156309.1; Identities = 491/504 (97 %), 5 gaps (0 %)) and *Pidoplitchkoviella terricola* (GenBank MH861046.1; Identities = 457/498 (92 %), 8 gaps (1 %)).

Falcocladium africanum Crous, *sp. nov.*

Etymology. Name refers to Africa, the continent where this fungus was collected.

Classification — *Falcocladiaceae*, *Falcocladiales*, *Sordariomycetes.*

Conidiophores penicillate, mostly synnematal, becoming sporodochial in older cultures, arising from superficial mycelium; stipe extensions hyaline, numerous per conidiophore, aseptate, thick-walled, 25–50 × 1.5–2.5 µm, arising from various positions in the conidiophore, terminating in vesicles that are sphaeropedunculate, to having lateral walls slightly flattened or even constricted, 4(–6) µm diam. *Conidiophore branches* primary branches hyaline, smooth, subcylindrical, 0–1-septate, 5–10 × 2–3 µm; secondary and tertiary branches hyaline, aseptate, 7–10 × 2–3 µm. *Conidiogenous cells* phialidic, in whorls of 2–6, ampulliform with elongated necks and periclinal thickening and minute collarettes, 7–11 × 2–3 µm. *Conidia* hyaline, smooth, 0–1-septate, falcate with a short, acute, thick-walled apical beak, and a basal appendage, (12–)15–18(–20) × 2(–2.5) µm; basal appendages exogenous on inner, shorter curve, 1.5–2 µm long, terminating in a rounded end; apical beak continuous with conidium body, 1.5–2 µm long.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white to buff, reverse buff.

Typus. Ghana, on leaves of *Eucalyptus brassiana* (*Myrtaceae*), June 2010, *M.J. Wingfield*, HPC 2177 (holotype CBS H-23787, culture ex-type CPC 34050 = CBS 145045, ITS, LSU, *actA* and *rpb2* sequences GenBank MK047418.1, MK047469.1, MK047518.1 and MK047532.1, MycoBank MB828166).

Additional materials examined. Sierra Leone, on leaves of *Eucalyptus tereticornis*, June 2010, *M.J. Wingfield*, HPC 2169, CPC 34017 = CBS 145046, ITS, LSU, *actA* and *rpb2* sequences GenBank MK047419.1, MK047470.1, MK047519.1 and MK047533.1; on leaves of *Eucalyptus brassiana* (*Myrtaceae*), June 2010, *M.J. Wingfield*, HPC 2166, CPC 34007, ITS and LSU sequences GenBank MK047420.1 and MK047471.1.

Notes — *Falcocladium* represents a genus of hyphomycetes associated with leaf litter, or considered to be weak foliar pathogens of *Eucalyptus* (Crous et al. 1994, 1997). Four species are presently known in the genus, having been collected on eucalypt leaves in Asia, Australia and South America. *Falcocladium africanum* represents the first species described from Africa, and differs from *F. thailandicum* (sphaeropedunculate vesicles, 6–7 µm diam, aseptate conidia, (19–)20–23(–24) × 1.5(–2) µm; Crous et al. 2007b) in vesicle shape, and having smaller, 0–1-septate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34050 had highest similarity to *Falcocladium thailandicum* (GenBank NR_156241.1; Identities = 638/656 (97 %), 6 gaps (0 %)), *Falcocladium sphaeropedunculatum* (GenBank EU040220.1; Identities = 567/661 (86 %), 43 gaps (6 %)) and *Falcocladium multivesiculatum* (GenBank JF831936.1; Identities = 420/466 (90 %), 15 gaps (3 %)). The ITS sequences of CPC 34007, 34017 and 34050 are identical. Closest hits using the ***rpb2*** sequence of CPC 34050 had only distant hits with *Fusarium* species (less than 80 % sequence similarity). The *rpb2* sequences of CPC 34017 and 34050 are identical as no other *rpb2* sequences are available for *Falcocladium* species.

Colour illustrations. *Eucalyptus tereticornis* plantation; Left column, *Castanediella tereticornis*, symptomatic leaf, conidiogenous cells and conidia. Right column, *Falcocladium africanum*, symptomatic leaf, conidiophore with stipe extension, vesicle and conidiogenous cells, and conidia. Scale bars = 10 µm.

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Zasmidium corymbiae

Fungal Planet 787 – 14 December 2018

Zasmidium corymbiae Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Submerged hyphae smooth, hyaline, thin-walled, 2.5–3 µm wide; *aerial hyphae* pale brown, verrucose, 3–4 µm diam, encased in mucoid layer. *Conidiophores* arising vertically from creeping aerial hyphae, brown, verruculose, thick-walled, 1–4-septate, 30–60 × 3–4 µm. *Conidiogenous cells* integrated, terminal, cylindrical, with slight apical taper, 10–20 × 0.5–2 µm long, pale brown, proliferating sympodially, forming a rachis with slightly thickened and darkened, circular, somewhat protruding scars, c. 0.5 µm diam. *Conidia* solitary, aseptate, finely roughened, pale brown, oblong to ellipsoidal, (4–)5–6(–7) × (2–)2.5(–3) µm, with obtuse apex and truncate unthickened, non-pigmented base.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium, copious mucoid droplets, and smooth, lobate margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey. On PDA surface and reverse iron-grey. On OA surface olivaceous grey.

Typus. Australia, New South Wales, Jackadgery, Inglebar Plantation, on leaves of *Corymbia citriodora* (*Myrtaceae*), 18 Mar. 2015, *A.J. Carnegie*, HPC 2031 (holotype CBS H-23751, culture ex-type CPC 33349 = CBS 145047, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047421.1, MK047472.1, MK047520.1, MK047524.1, MK047534.1 and MK047555.1, MycoBank MB828167).

Additional material examined. Australia, New South Wales, Jackadgery, Inglebar Plantation, on leaves of *C. citriodora*, 18 Mar. 2015, *A.J. Carnegie*, CPC 33350 = CBS 145048, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047422.1, MK047473.1, MK047521.1, MK047525.1, MK047535.1 and MK047556.1; ibid., CPC 33640 = CBS 145049, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047423.1, MK047474.1, MK047522.1, MK047526.1, MK047536.1 and MK047557.1.

Notes — *Zasmidium* and allied genera (*Periconiella*, ramichloridium-like, rasutoria-like, stenella-like, *Verrucisporota*) were recently revised by Videira et al. (2017), who presented an emended, wider circumscription of *Zasmidium* than that previously accepted by Braun et al. (2013). Several species are known to be associated with leaf spots on *Eucalyptus*, which are allied, but phylogenetically distinct from *Z. corymbiae*, which is more ramichloridium-like in morphology, having a terminal rachis on its conidiogenous cells, and aseptate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 33349 had highest similarity to *Zasmidium strelitziae* (GenBank NR_156514.1; Identities = 509/543 (94 %), 13 gaps (2 %)), *Zasmidium commune* (GenBank KY979762.1; Identities = 503/542 (93 %), 10 gaps (1 %)) and *Zasmidium pseudovespa* (GenBank NR_137548.1; Identities = 473/513 (92 %), 10 gaps (1 %)). The ITS sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the **LSU** sequence of CPC 33349 are *Zasmidium anthuriicola* (GenBank FJ839662.2; Identities = 831/846 (98 %), 2 gaps (0 %)), *Zasmidium citri* (GenBank GQ852733.1; Identities = 830/845 (98 %), 2 gaps (0 %)) and *Zasmidium citri-griseum* (GenBank KP895903.1; Identities = 823/838 (98 %), 2 gaps (0 %)). The LSU sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***actA*** sequence of CPC 33349 had highest similarity to *Zasmidium commune* (GenBank KY979857.1; Identities = 555/585 (95 %), 9 gaps (1 %)), *Zasmidium podocarpi* (GenBank KY979861.1; Identities = 548/600 (91 %), 14 gaps (2 %)) and *Zasmidium musae* (as *Stenella musae*, GenBank EU514347.1; Identities = 494/540 (91 %), 6 gaps (1 %)). The *actA* sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***cmdA*** sequence of CPC 33349 had highest similarity to *Zasmidium cellare* (GenBank MH591756.1; Identities = 281/306 (92 %), no gaps), *Acrodontium crateriforme* (GenBank KX289012.1; Identities = 280/305 (92 %), no gaps) and *Zasmidium pseudovespa* (as *Mycosphaerella pseudovespa*, GenBank KF902548.1; Identities = 269/290 (93 %), no gaps). The *cmdA* sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***rpb2*** sequence of CPC 33349 had highest similarity to *Zasmidium citri-griseum* (GenBank MF951696.1; Identities = 765/916 (84 %), 8 gaps (0 %)), *Zasmidium indonesianum* (GenBank MF951710.1; Identities = 758/915 (83 %), 6 gaps (0 %)) and *Zasmidium cerophillum* (GenBank MF951694.1; Identities = 756/913 (83 %), 4 gaps (0 %)). The *rpb2* sequences of CPC 33349, 33350 and 33640 are identical. Only distant hits with *Pseudocercospora* species were obtained when the ***tef1*** sequence was used in blast searches. The *tef1* sequences of CPC 33350 and 33640 are identical, while CPC 33349 differs from them at 1 nt.

Colour illustrations. *Corymbia citriodora* plantation in Australia; colony on potato dextrose agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Harknessia corymbiicola

Fungal Planet 788 – 14 December 2018

Harknessia corymbiicola Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes.*

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, multilocular, up to 2 mm diam, individual locules 100–300 µm diam; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner conidiomatal cavity. *Conidiogenous cells* 6–12 × 5–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (26–)28–32(–35) × (7–)8(–9) µm *in vitro*, fusoid with apiculus, aseptate, non-striate, medium brown, thick-walled, smooth-walled, granular to finely guttulate. *Basal appendage* (50–)65–80(–90) × 3(–4) µm *in vitro*, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* not seen.

Culture characteristics — Colonies flat, spreading, with fluffy moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white to buff, reverse cinnamon.

Typus. Australia, New South Wales, Grafton, Bom Bom State Forest, leaf litter of *Corymbia maculata* (*Myrtaceae*), 13 Mar. 2015, *A.J. Carnegie*, HPC 2034 (holotype CBS H-23752, culture ex-type CPC 33289 = CBS 145051, ITS, LSU and *tub2* sequences GenBank MK047424.1, MK047475.1 and MK047576.1, MycoBank MB828168).

Notes — *Harknessia* (*Harknessiaceae*; Crous et al. 2012a) is a genus of appendaged coelomycetous fungi that is commonly isolated from *Myrtaceae* and *Proteaceae. Harknessia* was treated by Marin-Felix et al. (2019), who accepted 38 species, recognising the majority as either endophytes, saprobes or foliar pathogens of minor importance. *Harknessia corymbiicola* represents a phylogenetically distinct species in the *H. weresubiae* species complex, being characterised by fusoid, apiculate conidia that lack striations, and have (50–)65–80(–90) µm long basal appendages.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Harknessia platyphyllae* (GenBank NR_155191.1; Identities = 625/640 (98 %), 11 gaps (1 %)), *Harknessia banksiae* (GenBank NR_155188.1; Identities = 625/641 (98 %), 5 gaps (0 %)) and *Harknessia banksiigena* (GenBank NR_155189.1; Identities = 614/630 (97 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Aurantiosacculus acutatus* (GenBank NG_042618.1; Identities = 840/843 (99 %), no gaps), *Harknessia ellipsoidea* (GenBank MH877405.1; Identities = 839/843 (99 %), no gaps) and *Harknessia pellitae* (GenBank KY979843.1; Identities = 839/843 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Harknessia eucalyptorum* (GenBank JQ706136.1; Identities = 615/651 (94 %), 11 gaps (1 %)), *Harknessia fusiformis* (GenBank JQ706139.1; Identities = 614/655 (94 %), 12 gaps (1 %)) and *Harknessia renispora* (GenBank AY720769.1; Identities = 609/652 (93 %), 9 gaps (1 %)).

Colour illustrations. *Corymbia maculata*, Bom Bom State Forest, Australia; Colony on oatmeal agar, conidiogenous cells and conidia with long basal appendages. Scale bars = 10 µm.

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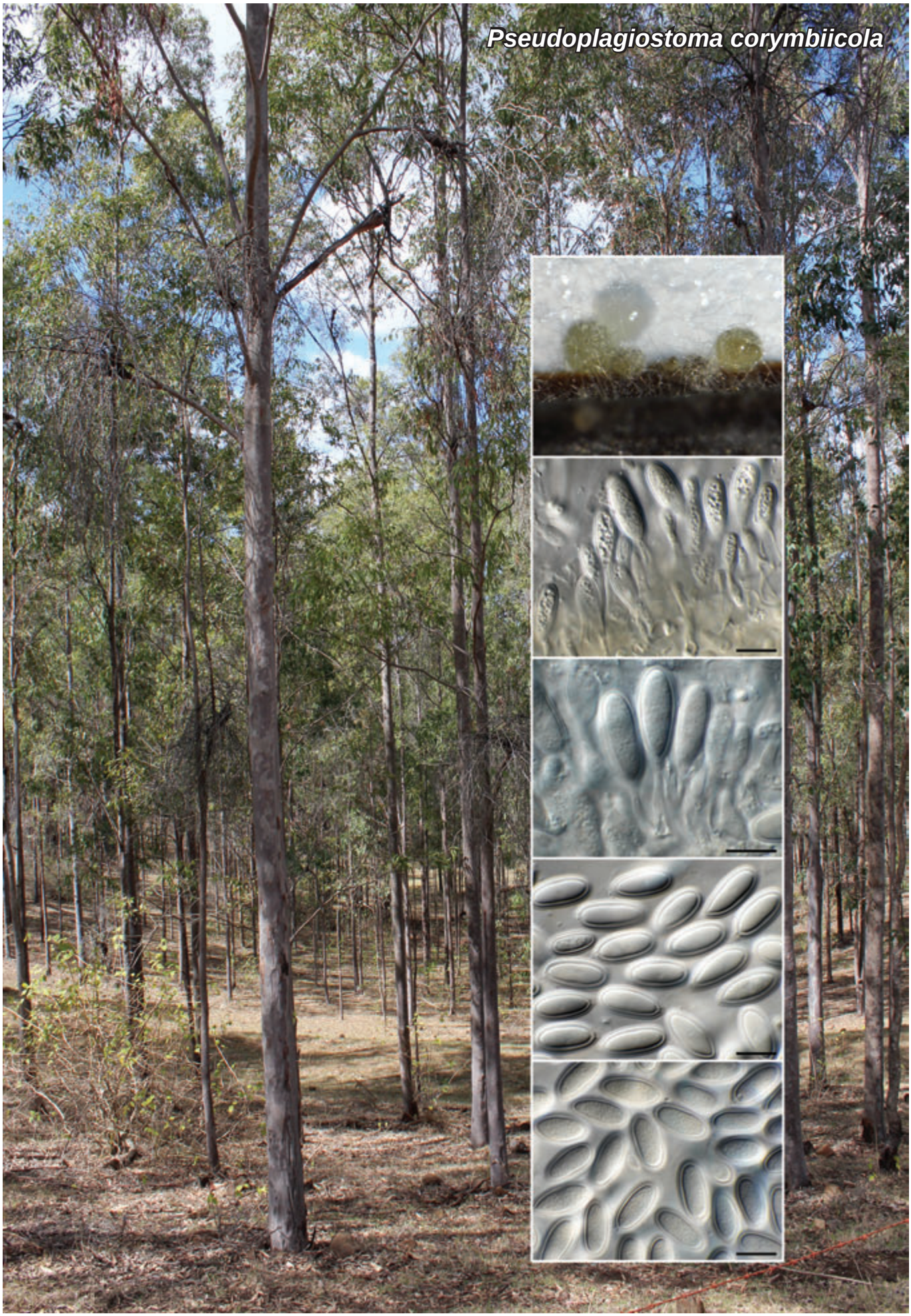
Pseudoplagiostoma corymbiicola

Fungal Planet 789 – 14 December 2018

Pseudoplagiostoma corymbiicola Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Pseudoplagiostomataceae*, *Diaporthales*, *Sordariomycetes.*

Conidiomata amphigenous on leaves, acervular, subcuticular to subepidermal, brown, separate; wall consisting of 2–3 layers of brown *textura angularis*, up to 300 µm diam; dehiscence by means of irregular slits; exuding white to cream conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, discrete, cylindrical to ampulliform with long cylindrical neck, hyaline, smooth, straight to curved, proliferating several times percurrently near apex, 15–30 × 3–5 µm. *Conidia* aseptate, hyaline, smooth, thick-walled, (1–2 µm diam), guttulate, elongate ellipsoidal, straight, apex broadly obtuse, tapering at base to a truncate hilum (1 µm diam), with minute marginal frill, (15–)16–17(–20) × (6–)7(–8) µm; encased in mucoid sheath (visible in Shear's mountant, less so in lactic acid).

Culture characteristics — Colonies flat, spreading, with fluffy, moderate aerial mycelium and feathery, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey with dirty white margin, reverse umber in centre, luteous in outer region. On PDA surface dirty white to buff, reverse pale olivaceous. On OA surface dirty white to buff.

Typus. Australia, New South Wales, Dyraaba, Dyraaba plantation, on leaves of *Corymbia citriodora*, 14 Mar. 2015, *A.J. Carnegie*, HPC 2027 (holotype CBS H-23753, culture ex-type CPC 33275= CBS 145052, ITS, LSU, *tef1* and *tub2* sequences GenBank MK047425.1, MK047476.1, MK047558.1 and MK047577.1, MycoBank MB828169).

Notes — The genus *Pseudoplagiostoma* (*Pseudoplagiostomaceae*; *Diaporthales*) presently contains five species, all of which are considered to be foliar pathogens (Cheewangkoon et al. 2010). *Pseudoplagiostoma corymbiicola* (conidia (15–)16–17(–20) × (6–)7(–8) µm) is morphologically closest to *P. corymbiae* (conidia (14–)16–18(–19) × (7–)8–9(–10) µm; Crous et al. 2012b), although conidia of the latter species are slightly wider, and the two species are also phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudoplagiostoma eucalypti* (GenBank GU973508.1; Identities = 561/569 (99 %), 3 gaps (0 %)), *Pseudoplagiostoma oldii* (GenBank GU973534.1; Identities = 560/569 (98 %), 4 gaps (0 %)) and *Pseudoplagiostoma variabile* (GenBank GU973536.1; Identities = 559/569 (98 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Pseudoplagiostoma corymbiae* (GenBank NG_042674.1; Identities = 834/840 (99 %), no gaps), *Juglanconis appendiculata* (GenBank KY427140.1; Identities = 812/841 (97 %), 2 gaps (0 %)), and *Pseudovalsa modonia* (GenBank MH875180.1; Identities = 811/840 (97 %), 1 gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudoplagiostoma variabile* (GenBank GU973566.1; Identities = 311/332 (94 %), 3 gaps (0 %)), *Pseudoplagiostoma eucalypti* (GenBank GU973540.1; Identities = 303/332 (91 %), 4 gaps (1 %)) and *Pseudoplagiostoma oldii* (GenBank GU973564.1; Identities = 301/333 (90 %), 5 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Pseudoplagiostoma variabile* (as *Diaporthales* sp. CR-2010b, GenBank GU993863.1; Identities = 461/470 (98 %), no gaps), *Pseudoplagiostoma oldii* (as *Diaporthales* sp. CR-2010a, GenBank GU993862.1; Identities = 451/469 (96 %), no gaps) and *Pseudoplagiostoma eucalypti* (GenBank AB978372.1; Identities = 446/470 (95 %), no gaps).

Colour illustrations. *Corymbia citriodora*, Dyraaba plantation, Australia; conidiomata sporulating on pine needle agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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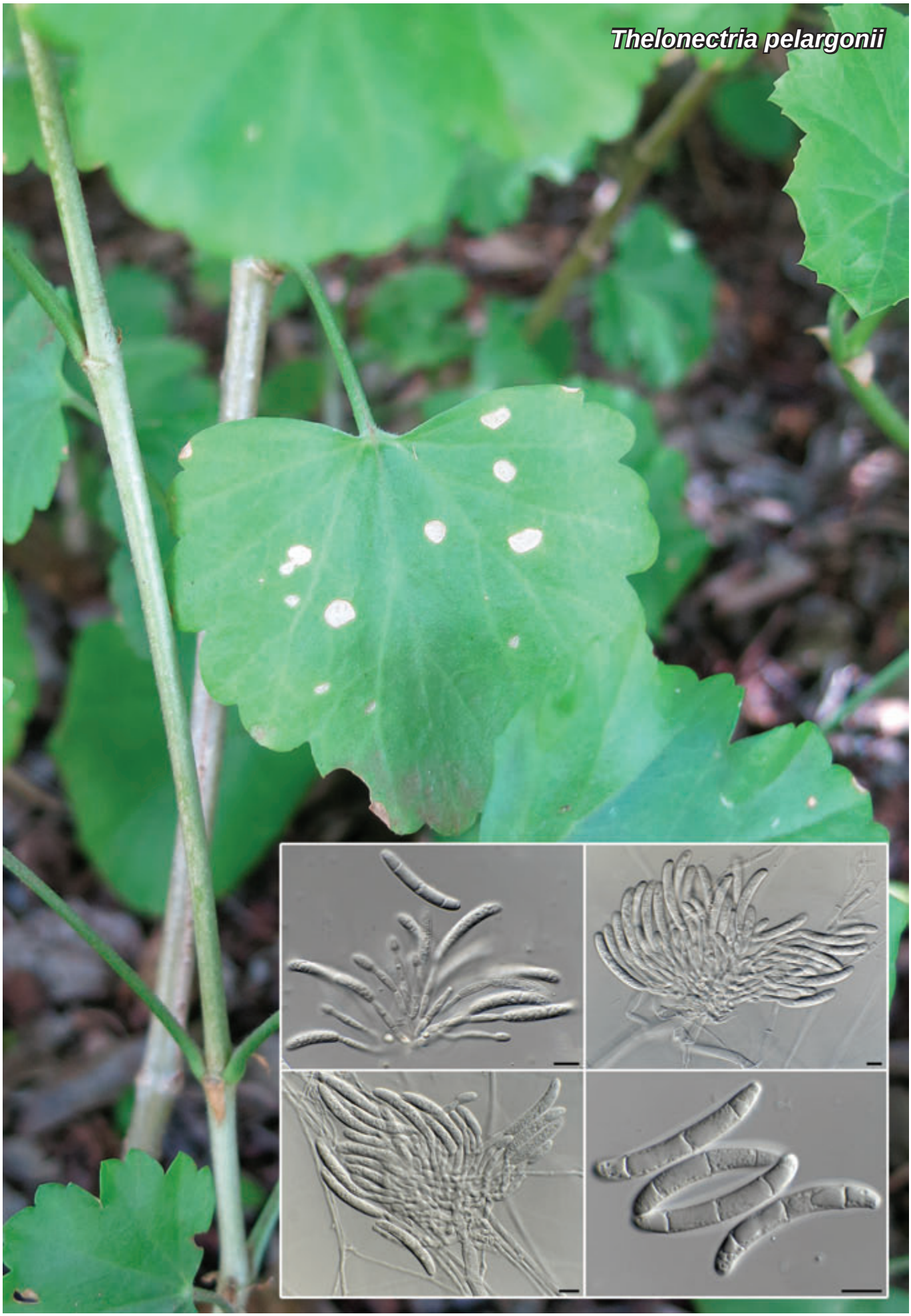
Thelonectria pelargonii

Fungal Planet 790 – 14 December 2018

Thelonectria pelargonii Crous, *sp. nov.*

Etymology. Name refers to *Pelargonium*, the host genus from which this fungus was isolated.

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3.5 µm diam hyphae. *Conidiomata* sporodochial, sessile on agar, 50–200 µm diam, basal stroma of cells arising from wide hyphae, 8–15 µm diam, giving rise to tightly aggregated cluster of primary branches, aseptate, 10–20 × 4–7 µm, forming several secondary branches, 10–15 × 4–5 µm, giving rise to erect, tertiary and quarterly branches, 10–17 × 3–4 µm, forming 1–3 cymbiform to subcylindrical phialides with periclinal thickening, 12–25 × 3.5–4 µm. *Conidia* solitary, curved, subcylindrical with obtuse ends, hyaline, smooth, guttulate, 3–4-septate, (41–)43–45(–47) × (6–)6.5(–7) µm. *Chlamydospores* and *ascomata* not seen.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse sienna to saffron. On PDA surface umber with diffuse sienna pigment, reverse umber. On OA surface sienna in centre, amber in outer region.

Typus. South Africa, Western Cape Province, Stellenbosch, *Pelargonium* sp. (*Geraniaceae*), 1 Feb. 2010, *P.W. Crous* (holotype CBS H-23754, culture ex-type CBS 145054, ITS, LSU, *his3*, *rpb2* and *tub2* sequences GenBank MK047426.1, MK047477.1, MK047530.1, MK047537.1 and MK047578.1, MycoBank MB828170).

Notes — The genus *Thelonectria* was established for a genus of *Nectriaceae* with cylindrocarpon-like asexual morphs (Chaverri et al. 2011) and presently includes approximately 40 species that are known to be saprobes or pathogens of hardwood trees and shrubs. *Thelonectria pelargonii*, which is phylogenetically distinct from other species in the genus, was associated with roots of a *Pelargonium* sp. in South Africa, but presently nothing is known about its ecology.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thelonectria veuillotiana* (GenBank KJ022014.1; Identities = 462/493 (94 %), 14 gaps (2 %)), *Thelonectria westlandica* (GenBank JQ403327.1; Identities = 480/515 (93 %), 11 gaps (2 %)) and *Cylindrocarpon olidum* (GenBank KC427020.1; Identities = 515/566 (91 %), 29 gaps (5 %)). Closest hits using the **LSU** sequence are *Thelonectria veuillotiana* (GenBank KJ022063.1; Identities = 818/829 (99 %), 1 gap (0 %)), *Thelonectria westlandica* (GenBank JQ403366.1; Identities = 807/824 (98 %), 1 gap (0 %)) and *Pleiocarpon strelitziae* (GenBank KY304672.1; Identities = 803/821 (98 %), 1 gap (0 %)). Closest hits using the ***his3*** sequence had highest similarity to *Thelonectria olida* (GenBank KM231487.1; Identities = 345/379 (91 %), 9 gaps (2 %)), *Penicillifer pulcher* (GenBank KM231456.1; Identities = 412/487 (85 %), 28 gaps (5 %)) and *Thelonectria discophora* (GenBank KM231489.1; Identities = 413/490 (84 %), 25 gaps (5 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Thelonectria lucida* (GenBank HQ897734.1; Identities = 798/870 (92 %), no gaps), *Thelonectria trachosa* (GenBank KM232343.1; Identities = 775/861 (90 %), no gaps) and *Acremonium macroclavatum* (GenBank HQ897740.1; Identities = 772/870 (92 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Thelonectria westlandica* (GenBank HM352868.1; Identities = 564/612 (92 %), 6 gaps (0 %)), *Thelonectria lucida* (GenBank KJ022321.1; Identities = 473/515 (92 %), 7 gaps (1 %)) and *Coccinonectria pachysandricola* (GenBank KM232033.1; Identities = 549/626 (88 %), 21 gaps (3 %)).

Colour illustrations. *Pelargonium* sp. growing in South Africa; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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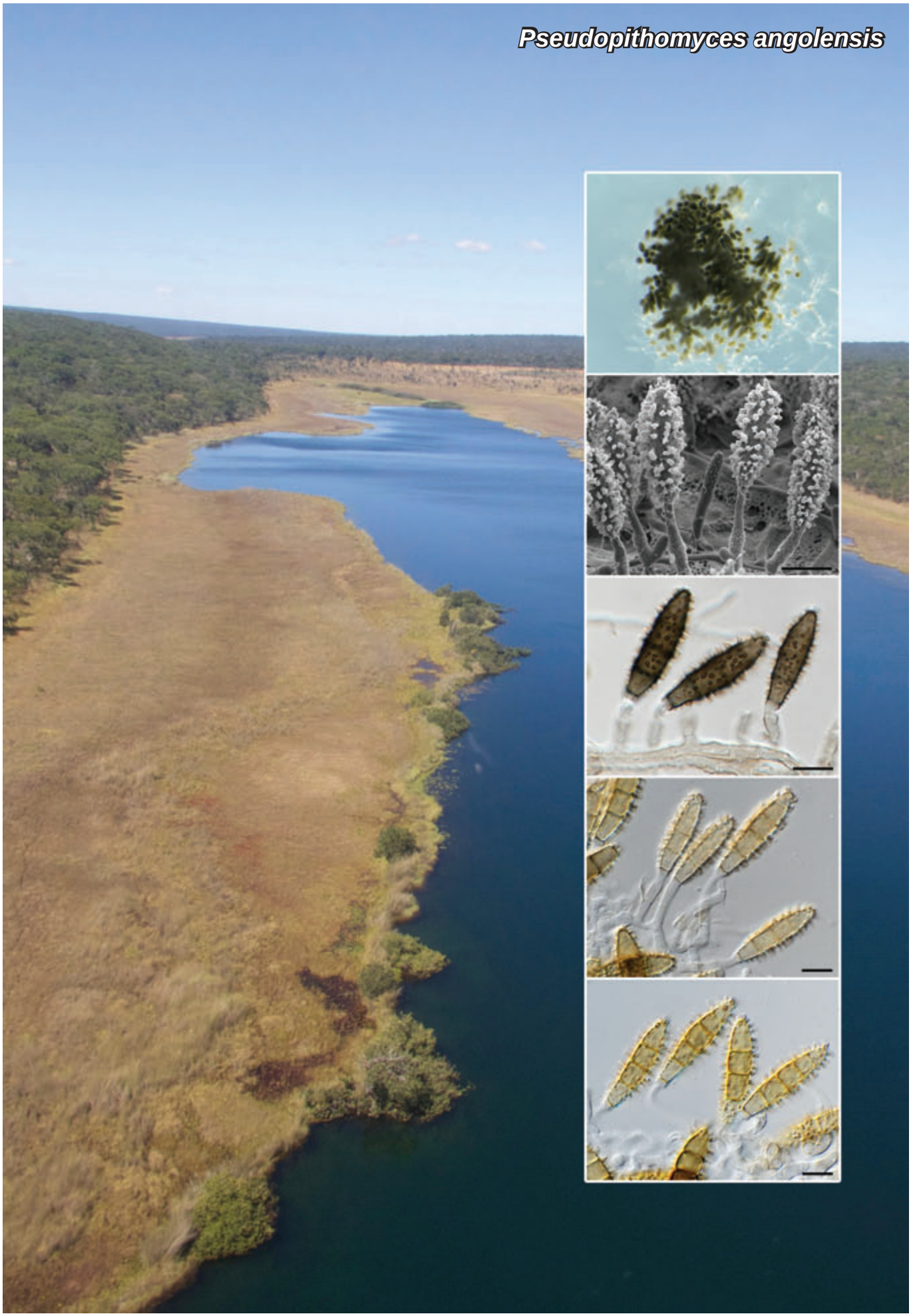
Pseudopithomyces angolensis

Fungal Planet 791 – 14 December 2018

Pseudopithomyces angolensis Crous, *sp. nov.*

Etymology. Name refers to Angola, the country where this species was collected.

Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of hyaline, septate, branched, 2–3.5 µm diam hyphae. *Conidiophores* solitary on aerial mycelium, but also becoming aggregated on agar surface, giving rise to sporodochia, up to 250 µm diam; conidiophores subcylindrical, branched or not, 1–3-septate, 10–25 × 2–3.5 µm, pale brown, smooth to verruculose. *Conidiogenous cells* smooth, pale brown, subcylindrical, proliferating percurrently, 7–15 × 2–3.5 µm; conidiogenesis peculiar in that the tip of the conidiogenesis cell is covered by the basal cap attached to conidia, and this is free from the conidiogenous cell itself. In young conidiogenous cells the conidiogenous cell is swollen at the apex, and the basal conidial cap appears to be attached to the tip, but later it is clearly a cap covering the apex of the conidiogenous cell. *Conidia* solitary, medium to dark brown, narrowly fusoid, apex obtuse, base with basal cup-shaped brown appendage; 3-septate, with two central cells somewhat darker than the apical and basal cell, (28–) 30–34(–37) × (7–)8(–9) µm; wall covered in tubular warts, 1–3 × 1–1.5 µm (tubes open once mature); basal cap-like appendage brown, 2–3 × 3–4 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface mouse grey to olivaceous grey, reverse olivaceous grey.

Typus. Angola, Cuito Source Lake, leaf spot of unknown host plant, 13 Mar. 2014, *J. Roux*, HPC 2084 = NGA 242 (holotype CBS H-23756, culture extype CPC 33597 = CBS 145056, ITS, LSU and *rpb2* sequences GenBank MK047427.1, MK047478.1 and MK047538.1, MycoBank MB828171).

Notes — *Pseudopithomyces* contains around 10 species, distinguished from *Pithomyces* s.str. by having fusoid, echinulate to verruculose conidia that are visible as brown to black colonies on the host. In contrast, *Pithomyces* produces obovate to ovoid, verruculose, pale brown conidia that form whitish to yellowish colonies on the host (Ellis 1971). Colonies of *Pseudopithomyces angolensis* were small, black and shiny on leaves, and were initially assumed to represent packets of insect eggs. Morphologically, it is distinct from *P. chartarum* (conidia with 3 transverse and 1–2 vertical septa, 18–29 × 10–17 µm; Ellis 1971) in having longer, narrower conidia that lack vertical septa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had highest similarity to *Pithomyces chartarum* (strain CBS 485.71, GenBank MH860227.1; Identities = 596/601 (99 %), 1 gap (0 %)) and several other sequences labelled as *Pithomyces chartarum* or *Pseudopithomyces chartarum*; however, several other cultures of this species are more distant (e.g., CBS 805.72, CBS 679.71 and CBS 712.70, GenBank MH860611.1, MH860299.1 and MH859914.1; Identities = 588/607 (97 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Pseudopithomyces rosae* (GenBank NG_059876.1; Identities = 842/842 (100 %), no gaps), *Pseudopithomyces palmicola* (GenBank KU554628.1; Identities = 847/848 (99 %), no gaps) and *Pithomyces chartarum* (as *Leptosphaerulina chartarum*, GenBank LK936376.1; Identities = 847/848 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Pithomyces chartarum* (as *Leptosphaerulina chartarum*, GenBank LK936415.1; Identities = 895/935 (96 %), 2 gaps (0 %)), *Sporidesmiella fusiformis* (GenBank DQ435079.1; Identities = 681/729 (93 %), 2 gaps (0 %)) and *Pseudopithomyces maydicus* (as *Pithomyces maydicus*, GenBank LK936419.1; Identities = 832/926 (90 %), 3 gaps (0 %)).

Colour illustrations. Cuito Source Lake, Angola; colony on synthetic nutrient poor agar, Scanning Electron Micrograph of conidia (photo: Jan Dijksterhuis), conidiogenous cells and conidia. Scale bars = 10 µm.

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Gnomoniopsis angolensis

Fungal Planet 792 – 14 December 2018

Gnomoniopsis angolensis Crous, *sp. nov.*

Etymology. Name refers to Angola, the country where this fungus was collected.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes.*

Conidiomata solitary, eustromatic, mono- to multilocular, with central ostiole, pycnidial, exuding a creamy conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline to subhyaline at base, subcylindrical with prominent apical taper, 0–2-septate, branched at base, 15–25 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform to cymbiform, terminal and intercalary, 10–15 × 2–3 µm, phialidic. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex obtuse, tapering at base to truncate hilum, 0.5 µm diam, straight to slightly curved, aseptate, (8–)9–10(–11) × 2(–2.5) µm.

Culture characteristics — Colonies spreading, with sparse to moderate aerial mycelium and even, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface sienna with zones of dirty white, reverse sienna with zones of luteous. On PDA surface greyish sepia, reverse pale mouse grey. On OA surface pale mouse grey.

Typus. Angola, Cuanavale Source Lake, 1354 m, leaf spot of unknown host plant, 16 Mar. 2010, *J. Roux*, HPC 2080, NGA 315, WP1397 (holotype CBS H-23757, culture ex-type CPC 33595 = CBS 145057, ITS, LSU and *rpb2* sequences GenBank MK047428.1, MK047479.1 and MK047539.1, MycoBank MB828172).

Notes — *Gnomoniopsis* contains c. 15 species, most of which are endophytic or pathogenic to species of *Fagaceae*, *Onagraceae* and *Rosaceae* (Crous et al. 2012b). *Gnomoniopsis angolensis* is phylogenetically distinct from known species (Walker et al. 2010).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gnomoniopsis smithogilvyi* (GenBank KC145878.1; Identities = 576/600 (96 %), 10 gaps (1 %)), *Discula quercina* (GenBank GQ452265.1; Identities = 571/597 (96 %), 6 gaps (1 %)) and *Gnomoniopsis castaneae* (GenBank MH384925.1; Identities = 564/590 (96 %), 10 gaps (1 %)). Closest hits using the **LSU** sequence are *Gnomoniopsis smithogilvyi* (GenBank MH877030.1; Identities = 837/841 (99 %), no gaps), *Allantophoma endogenospora* (GenBank EU754126.1; Identities = 835/839 (99 %), no gaps) and *Gnomoniopsis castaneae* (GenBank KX929802.1; Identities = 828/832 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Gnomoniopsis clavulata* (GenBank EU219242.1; Identities = 809/869 (93 %), no gaps), *Gnomoniopsis paraclavulata* (GenBank EU219248.1; Identities = 793/870 (91 %), no gaps) and *Discula campestris* (GenBank EU199143.1; Identities = 792/869 (91 %), no gaps).

Colour illustrations. Cuanavale Source Lake in Angola; symptomatic leaf, colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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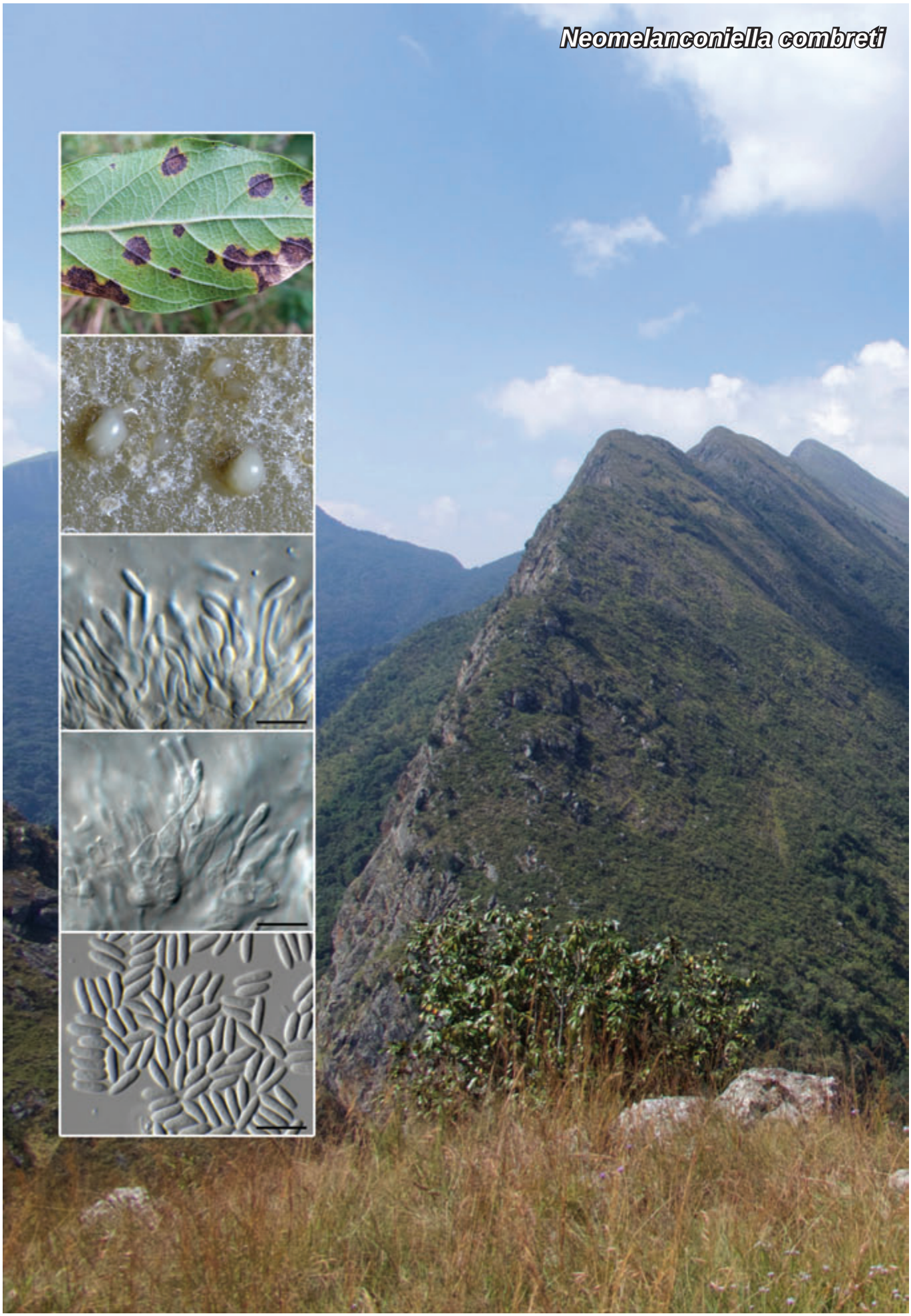
Neomelanconiella combreti

Fungal Planet 793 – 14 December 2018

Neomelanconiellaceae Crous, *fam. nov.*

MycoBank MB828247.

Neomelanconiella Crous, *gen. nov.*

Etymology. Name refers to *Melanconiella*, a genus which is morphologically similar.

Classification — *Neomelanconiellaceae*, *Diaporthales*, *Sordariomycetes*.

Conidiomata solitary to aggregated, pycnidial, brown with central ostiole; wall of 3–6 layers of medium brown *textura angularis. Conidiophores* lining the inner cavity, septate, hyaline, smooth, subcylindrical with slight apical taper, branched or not. *Conidiogenous cells* hyaline, smooth, ampulliform, terminal and intercalary, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum.

Type species. *Neomelanconiella combreti* Crous.
MycoBank MB828246.

Notes — The family *Neomelanconiellaceae* presently only includes *Neomelanconiella*, and clusters between *Melanconiellaceae* and *Harknessiaceae*.

Neomelanconiella combreti Crous, *sp. nov.*

Etymology. Name refers to *Combretum*, the host genus from which this fungus was isolated.

Conidiomata solitary to aggregated, pycnidial, 200–250 µm diam, brown with central ostiole; wall of 3–6 layers of medium brown *textura angularis. Conidiophores* lining the inner cavity, 1–2-septate, hyaline, smooth, subcylindrical with slight apical taper, branched or not, 10–20 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform, terminal and intercalary, 7–12 × 2.5–3 µm, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum, 1 µm diam, (6–)7–8 × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and folded surface, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse buff. On PDA surface ochreous, reverse pale luteous. On OA surface pale luteous.

Typus. South Africa, Limpopo Province, Haenertsburg, Wolkberg, Klipdraai Camp, leaf spot on *Combretum* sp. (*Combretaceae*), 30 Mar. 2010, *J. Roux*, HPC 2089 (holotype CBS H-23758, culture ex-type CPC 33664 = CBS 145058, ITS, LSU, *rpb2* and *tef1* sequences GenBank MK047429.1, MK047480.1, MK047540.1 and MK047559.1, MycoBank MB828173).

Colour illustrations. Wolkberg, South Africa; symptomatic leaf, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Melanconiella* presently includes approximately 20 species (Voglmayr et al. 2012), most of which occur on recently dead twigs and branches of *Betulaceae*, occurring in the north temperate zone. Asexual morphs of *Melanconiella* have in the past been described in *Melanconium*, although the latter genus is in need of revision (Sutton 1980). Morphologically, there is little to choose between *Melanconiella* and *Neomelanconiella*, although *N. combreti* occurs on leaves of *Combretaceae*, and in the Southern Hemisphere. *Neomelanconiella combreti* clusters with an isolate identified as *Cryptodiaporthe vepris* (AR 3559, on *Rubus idaeus* (*Rosaceae*), Austria), although the latter genus is now a synonym of *Plagiostoma* (Mejía et al. 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Melanconiella ellisii* (GenBank JQ926269.1; Identities = 404/449 (90 %), 22 gaps (5 %)), *Sphaeronaemella fragariae* (GenBank AY271808.1; Identities = 394/440 (90 %), 16 gaps (4 %)) and *Melanconiella spodiaea* (GenBank JQ926299.1; Identities = 400/448 (89 %), 20 gaps (4 %)). Closest hits using the **LSU** sequence are *Sphaeronaemella fragariae* (GenBank MH866172.1; Identities = 817/845 (97 %), 9 gaps (1 %)), *Cryptodiaporthe vepris* (GenBank EU683070.1; Identities = 816/844 (97 %), 8 gaps (0 %)) and *Harknessia fusiformis* (GenBank JQ706220.1; Identities = 815/843 (97 %), 6 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Melanconiella hyperopta* var. *orientalis* (GenBank JQ926352.1; Identities = 743/925 (80 %), 9 gaps (0 %)), *Cryphonectria parasitica* (GenBank DQ862017.1; Identities = 722/934 (77 %), 19 gaps (2 %)) and *Synnemasporella toxicodendri* (GenBank MG682049.1; Identities = 716/924 (77 %), 21 gaps (2 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Melanconiella ellisii* (GenBank JQ926406.1; Identities = 239/282 (85 %), 18 gaps (6 %)), *Tubakia suttoniana* (GenBank MG592106.1; Identities = 228/274 (83 %), 16 gaps (5 %)) and *Tubakia oblongispora* (GenBank MG592084.1; Identities = 231/279 (83 %), 24 gaps (8 %)).

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Monilochaetes melastomae

Fungal Planet 794 – 14 December 2018

Monilochaetes melastomae Crous, *sp. nov.*

Etymology. Name refers to *Melastoma*, the host genus from which this fungus was isolated.

Classification — *Australiascaceae*, *Chaetosphaeriales*, *Sordariomycetes.*

Mycelium consisting of pale brown, smooth to finely roughened, branched, septate, 2.5–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, brown, smooth, rarely branched at base, becoming paler brown toward apex, straight, 2–3(–8)-septate, 90–250 × 6–10 µm. *Conidiogenous cells* terminal, pale brown, smooth, subcylindrical with apical taper to truncate apex, 40–55 × 6–7 µm, phialidic with prominent periclinal thickening at apex, 3–4 µm diam. *Conidia* aseptate, occurring in unbranched chains (–30), ellipsoid to narrowly obovoid, hyaline, smooth, guttulate, apex obtuse, tapering at base to truncate hilum, 2 µm diam, (17–)18–19(–20) × (7.5–)8 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface fuscous black, reverse iron-grey. On PDA surface and reverse olivaceous grey. On OA surface olivaceous grey to iron-grey.

Typus. Malaysia, leaf spots of *Melastoma* sp. (*Melastomataceae*), 25 July 2017, *M.J. Wingfield*, HPC 2199 (holotype CBS H-23759, culture ex-type CPC 34181 = CBS 145059, ITS and LSU sequences GenBank MK047430.1 and MK047481.1, MycoBank MB828174).

Notes — *Monilochaetes* (sexual morph *Australiasca*) is a hyphomycetous genus with solitary, erect, sometimes curved or geniculate, dark brown conidiophores with prominently darkened septa, terminal, wide monophialides with a shallow collarette, and aseptate, rarely septate, hyaline conidia adhering in basipetal chains or heads (Réblová et al. 2011). Using the key of Réblová et al. (2011), *M. melastomae* is similar to *M. guadalcanalensis* (conidia 18–21 × 6–9 µm), although the former differs by forming shorter conidiophores and extremely long conidial chains, and is also phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Australiasca queenslandica* (GenBank KP204397.1; Identities = 463/472 (98 %), no gaps), *Monilochaetes nothapodytis* (GenBank MF153475.1; Identities = 476/499 (95 %), 9 gaps (1 %)) and *Australiasca laeensis* (GenBank EF029187.1; Identities = 506/547 (93 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Monilochaetes dimorphospora* (GenBank HQ609480.1; Identities = 899/907 (99 %), no gaps), *Monilochaetes guadalcanalensis* (GenBank MH872756.1; Identities = 887/895 (99 %), no gaps) and *Australiasca queenslandica* (GenBank HM237323.1; Identities = 898/907 (99 %), no gaps).

Colour illustrations. Symptomatic leaves of *Melastoma* sp. growing in Malaysia; conidial chains, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Dothiora corymbiae

Fungal Planet 795 – 14 December 2018

Dothiora corymbiae Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Dothideaceae*, *Dothideales*, *Dothideomycetes.*

Conidiomata pycnidial, separate, obovoid, papillate, brown, with central ostiole, 100–150 µm diam; wall of 4–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, ellipsoid, hyaline, polyphialidic, with 1–3 loci per conidiogenous cell, 5–10 × 4–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, straight, 4–5 × 2 µm; once discharged onto the agar surface, conidia turn brown, and become swollen, thick-walled, ellipsoid, 5–6 × 3–4 µm.

Culture characteristics — Colonies slimy, yeast-like, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface sepia, reverse hazel. On PDA surface and reverse sepia. On OA surface hazel to fawn.

Typus. Australia, Queensland, Minden, on leaves of *Corymbia citriodora* (*Myrtaceae*), 1 Feb. 2010, *J. Roux*, CJA010 (holotype CBS H-23760, isotype BRIP 58843a, culture ex-type CPC 33719 = CBS 145060, ITS and LSU sequences GenBank MK047431.1 and MK047482.1, MycoBank MB828175).

Colour illustrations. Indigenous forest in Queensland, Australia; colony sporulating on malt extract agar, conidioma, hyphae, conidiogenous cells and conidia. Scale bars: conidioma = 150 µm, all others = 10 µm.

Notes — *Dothiora* was recently treated by Crous & Groenewald (2016, 2017). *Ascostromata* were shown to lack pseudoparaphyses, have bitunicate asci with hyaline, transversely septate ascospores (rarely with vertical septa). Conidiomata are pycnidial, conidiophores reduced to hyaline, phialidic conidiogenous cells, and *conidia* aseptate, hyaline, smooth, subcylindrical to ovoid or oblong, forming a hormonema-like synasexual morph. The present collection is thus best accommodated in *Dothiora.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocylindroseptoria pistaciae* (GenBank KF251152.1; Identities = 512/577 (89 %), 37 gaps (6 %)), *Dothiora sorbi* (GenBank MH860401.1; Identities = 509/590 (86 %), 42 gaps (7 %)) and *Kabatina thujae* (GenBank MH858858.1; Identities = 484/555 (87 %), 38 gaps (6 %)). Closest hits using the **LSU** sequence are *Dothiora ceratoniae* (GenBank MH872233.1; Identities = 818/839 (97 %), 3 gaps (0 %)), *Dothiora schizospora* (GenBank MH868980.1; Identities = 817/839 (97 %), 2 gaps (0 %)) and *Dothiora cactacearum* (GenBank KY929177.1; Identities = 817/839 (97 %), 2 gaps (0 %)).

Dothiora Fr., Summa Veg. Scand., Sectio Post. (Stockholm): 418. 1849

Synonyms. *Cylindroseptoria* Thambug. & K.D. Hyde, Fung. Diversity 68: 125. 2014.
Neophaeocryptopus Wanas. et al., Fung. Diversity 78: 21. 2016.

For additional synonyms see Crous & Groenewald (2017).

Dothiora pistaciae (Quaedvlieg et al.) Crous, *comb. nov*.

MycoBank MB828176.

Basionym. *Cylindroseptoria pistaciae* Quaedvlieg et al., Stud. Mycol. 75: 359. 2013.

Synonym. *Neocylindroseptoria pistaciae* (Quaedvlieg et al.) Thambug. et al., Fung. Diversity 68: 125. 2014.

Dothiora mahoniae (A.W. Ramaley) Crous, *comb. nov*.

MycoBank MB828177.

Basionym. *Kabatina mahoniae* A.W. Ramaley, Mycotaxon 43: 443. 1992.

Dothiora cytisi (Wanas. et al.) Crous, *comb. nov*.

MycoBank MB828178.

Basionym. *Neophaeocryptopus cytisi* Wanas. et al., Fung. Diversity 78: 22. 2016.

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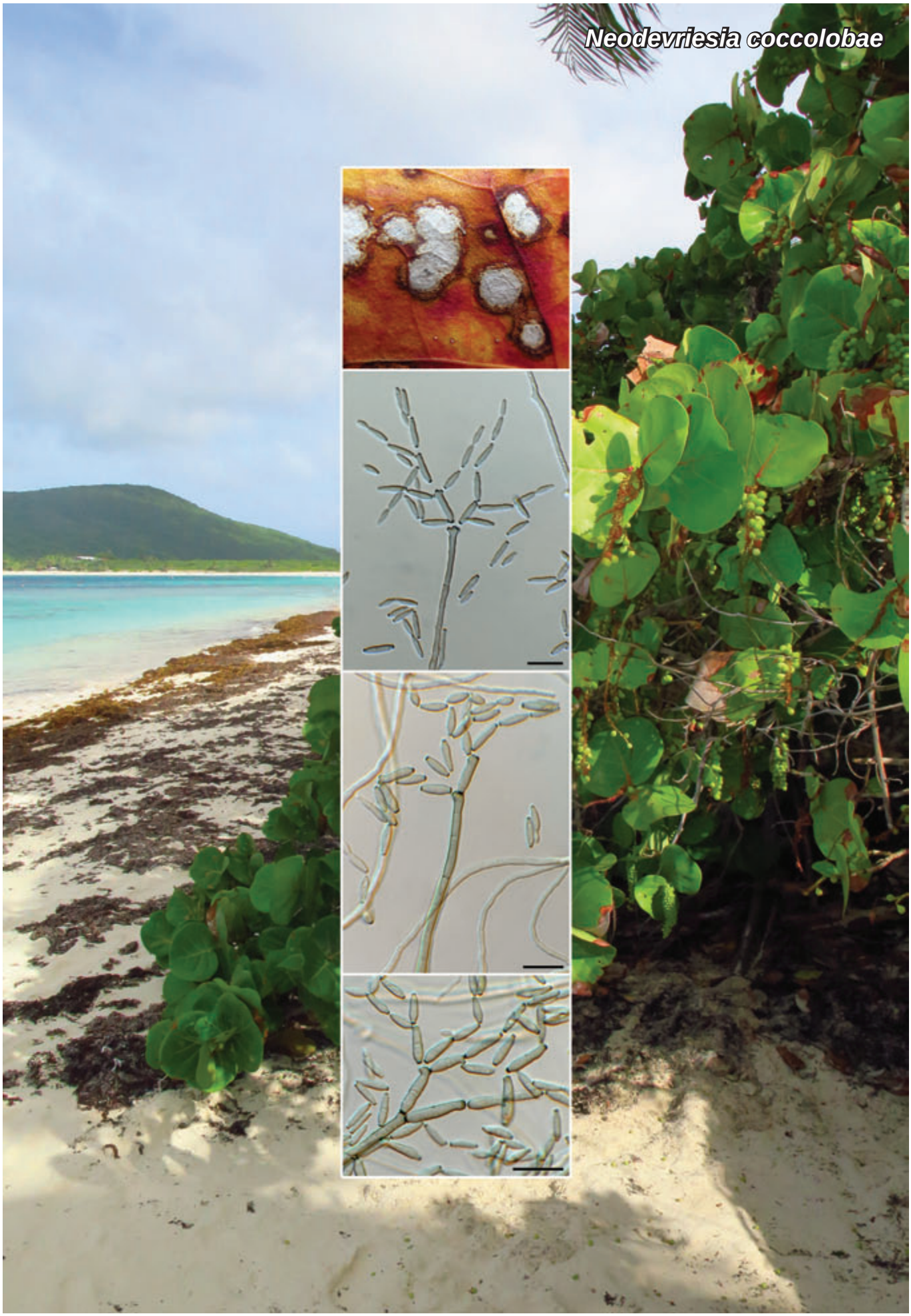
Neodevriesia coccolobae

Fungal Planet 796 – 14 December 2018

Neodevriesia coccolobae Crous, *sp. nov.*

Etymology. Name refers to *Coccoloba*, the host genus from which this fungus was isolated.

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of olivaceous, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* erect, mononematous, 1–5-septate, brown, smooth, subcylindrical, straight to flexuous, unbranched, 12–100 × 2.5–3.5 µm. *Conidiogenous cells* terminal, subcylindrical, brown, smooth, (7–)10–15 × (2–)2.5 µm, polyblastic, loci 1.5–2 µm diam, darkened. *Ramoconidia* 0(–1)-septate, subcylindrical, pale brown, smooth, 10–17 × 2.5–3.5 µm. *Conidia* in branched chains, 0(–1)-septate, pale brown, smooth, subcylindrical to narrowly fusoid, tapering at ends to truncate hila, 0.5–1 µm diam, (6–)7–8(–10) × (2–)2.5(–3) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA, surface and reverse olivaceous brown.

Typus. Puerto Rico, on leaves of *Coccoloba uvifera* (*Polygonaceae*), May 2017, *M.J. Wingfield*, HPC 2164 (holotype CBS H-23761, culture ex-type CPC 34073 = CBS 145064, ITS and LSU sequences GenBank MK047432.1 and MK047483.1, MycoBank MB828179).

Notes — Quaedvlieg et al. (2014) established *Neodevriesia* for a group of hyphomycetes with medium brown, unbranched conidiophores, thick-walled, medium brown, rarely septate conidia, occurring in short and mostly unbranched conidial chains, and lacking chlamydospores. *Neodevriesia* is generally plant-associated, and distinct from the mainly soil-inhabiting *Devriesia* s.str. *Neodevriesia coccolobae* is phylogenetically distinct from the approximately 20 species that are presently attributed to the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915745.1; Identities = 419/455 (92 %), 15 gaps (3 %)), *Scytalidium infestans* (GenBank MH873928.1; Identities = 481/526 (91 %), 9 gaps (1 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578112.1; Identities = 480/525 (91 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Neodevriesia cladophorae* (GenBank KU578114.1; Identities = 855/862 (99 %), no gaps), *Neodevriesia queenslandica* (as *Devriesia queenslandica*, GenBank JF951168.1; Identities = 889/899 (99 %), 4 gaps (0 %)) and *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915749.1; Identities = 880/890 (99 %), 4 gaps (0 %)).

Colour illustrations. Beach at Puerto Rico; symptomatic leaf, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Neodevriesia tabebuiae

Fungal Planet 797 – 14 December 2018

Neodevriesia tabebuiae Crous, *sp. nov.*

Etymology. Name refers to *Tabebuia*, the host genus from which this fungus was isolated.

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* erect, mononematous, 0–2-septate, brown, smooth, subcylindrical to geniculous-sinuous, unbranched, frequently reduced to conidiogenous loci on hyphae, 3–50 × 2–3 µm. *Conidiogenous cells* terminal, subcylindrical, pale brown, smooth, 3–15 × 2–3 µm, polyblastic, loci 1–1.5 µm diam, somewhat darkened and thickened. *Ramoconidia* 0–1-septate, subcylindrical, pale brown, smooth, 7–15 × 2–3 µm. *Conidia* in branched chains, 0–1-septate, pale brown, smooth to finely roughened, subcylindrical, tapering at ends to truncate hila, somewhat darkened, 1 µm diam, (6–)7–8(–10) × (2–)2.5(–3) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. Puerto Rico, on leaves of *Tabebuia chrysantha* (*Bignoniaceae*), May 2017, *M.J. Wingfield*, HPC 2178 (holotype CBS H-23762, culture ex-type CPC 34081 = CBS 145065, ITS and LSU sequences GenBank MK047433.1 and MK047484.1, MycoBank MB828180).

Notes — *Neodevriesia tabebuiae* and *N. coccolobae* were both collected from leaves of different plant species growing in Puerto Rico; however, their ITS sequences are only 94 % (498/532, including 2 gaps) similar. Phylogenetically, *N. tabebuiae* is distinct from the approximately 20 species that are presently attributed to *Neodevriesia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 519/572 (91 %), 21 gaps (3 %)), *Scytalidium infestans* (GenBank MH873928.1; Identities = 517/571 (91 %), 16 gaps (2 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578112.1; Identities = 507/561 (90 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Neodevriesia hilliana* (GenBank GU214414.1; Identities = 879/897 (98 %), 4 gaps (0 %)), *Neodevriesia shakazului* (GenBank NG_042753.1; Identities = 873/890 (98 %), 4 gaps (0 %)) and *Neodevriesia queenslandica* (as *Devriesia queenslandica*, GenBank JF951168.1; Identities = 879/899 (98 %), 4 gaps (0 %)).

Colour illustrations. Forest in Puerto Rico; conidiophores, conidiogenous cells and conidial chains. Scale bars = 10 µm.

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Alfaria tabebuiae

Fungal Planet 798 – 14 December 2018

Alfaria tabebuiae Crous, *sp. nov.*

Etymology. Name refers to *Tabebuia*, the host genus from which this fungus was isolated.

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiomata sporodochial, superficial, cupulate, scattered to gregarious, oval in outline, 100–300 µm diam, with slimy, olivaceous brown conidial masses. *Setae* flexuous, unbranched, thick-walled, apex subobtuse, dark brown, verruculose, 6–8-septate, 130–200 × 6–7 µm. *Conidiophores* arising from the basal stroma, densely aggregated, subcylindrical, 3–5-septate, branched, becoming pigmented and verruculose toward apex, 30–50 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, becoming pigmented and verruculose in upper region, phialidic with periclinal thickening and flared collarette, 10–15 × 2–2.5 µm. *Conidia* aseptate, solitary, fusoid-ellipsoid, straight, apex subobtuse, base truncate, 1.5–2 µm diam, guttulate, granular, olivaceous brown, smooth, (6–)7(–7.5) × (2.5–)3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, folded surface, and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface salmon, reverse orange. On PDA surface salmon, reverse pale luteous. On OA surface salmon.

Typus. Puerto Rico, on leaves of *Tabebuia chrysantha* (*Bignoniaceae*), May 2017, *M.J. Wingfield*, HPC 2178 (holotype CBS H-23763, culture ex-type CPC 34038 = CBS 145066, ITS, LSU, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047434.1, MK047485.1, MK047527.1, MK047541.1, MK047560.1 and MK047579.1, MycoBank MB828181).

Additional material examined. Puerto Rico, on leaves of *T. chrysantha*, May 2017, *M.J. Wingfield*, HPC 2178, CPC 34083 = CBS 145063, ITS, LSU, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047435.1, MK047486.1, MK047528.1, MK047542.1, MK047561.1 and MK047580.1.

Notes — *Alfaria* was established for a fungus causing a disease on *Cyperus esculentus* in Spain, and presently contains close to 20 species (Crous et al. 2014a, 2018a, Lombard et al. 2016). *Alfaria tabebuiae* is phylogenetically closely related to *A. acaciae* (conidia (6–)8–10(–12) × (2.5–)3 µm; Crous et al. 2018a), although it has shorter conidia, and longer setae. Several isolates identified as *Amerosporium* spp. cluster in the *Alfaria* clade. However, *Amerosporium* has unilocular, spherical conidiomata, and is distinct from the sporodochial conidiomata of *Alfaria*. Synapomorphies between the genera are pigmented setae, phialidic conidiogenous cells and pigmented, aseptate conidia. The morphology of these '*Amerosporium'* isolates will be resolved in a later study.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank NR_158363.1; Identities = 572/582 (98 %), 5 gaps (0 %)), *Alfaria cyperi-esculenti* (GenBank KJ869143.1; Identities = 575/591 (97 %), 10 gaps (1 %)) and *Alfaria thymi* (GenBank NR_154714.1; Identities = 568/587 (97 %), 13 gaps (2 %)). The ITS sequences of CPC 34038 and 34083 differ with 1 nt. Closest hits using the **LSU** sequence of CPC 34038 are *Alfaria acaciae* (GenBank MH107930.1; Identities = 857/859 (99 %), no gaps), *Alfaria cyperi-esculenti* (GenBank KJ869200.1; Identities = 801/804 (99 %), no gaps) and *Alfaria thymi* (GenBank KU845999.1; Identities = 822/828 (99 %), 1 gap (0 %)). The LSU sequences of CPC 34038 and 34083 are identical. Closest hits using the ***cmdA*** sequence of CPC 34038 had highest similarity to *Alfaria terrestris* (GenBank KU845979.1; Identities = 486/542 (90 %), 4 gaps (0 %)), *Alfaria acaciae* (GenBank MH107991.1; Identities = 530/611 (87 %), 7 gaps (1 %)) and *Gregatothecium humicola* (GenBank KU846285.1; Identities = 482/542 (89 %), 4 gaps (0 %)). The *cmdA* sequences of CPC 34038 and 34083 are identical. Closest hits using the ***rpb2*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108001.1; Identities = 653/702 (93 %), no gaps), *Alfaria thymi* (GenBank KU846006.1; Identities = 508/578 (88 %), no gaps) and *Alfaria caricicola* (GenBank KU846001.1; Identities = 521/597 (87 %), no gaps). The *rpb2* sequences of CPC 34038 and 34083 are identical. Closest hits using the ***tef1*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108013.1; Identities = 378/437 (86 %), 22 gaps (5 %)), *Alfaria caricicola* (GenBank KU846008.1; Identities = 324/403 (80 %), 16 gaps (3 %)) and *Alfaria terrestris* (GenBank KU846010.1; Identities = 309/378 (82 %), 28 gaps (7 %)). The *tef1* sequences of CPC 34038 and 34083 differ with 1 nt. Closest hits using the ***tub2*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108035.1; Identities = 400/425 (94 %), 4 gaps (0 %)), *Alfaria terrestris* (GenBank KU846019.1; Identities = 327/350 (93 %), 3 gaps (0 %)) and *Alfaria putrefolia* (GenBank KU846017.1; Identities = 325/349 (93 %), 1 gap (0 %)). The *tub2* sequences of CPC 34038 and 34083 differ with 2 nt.

Colour illustrations. Forest in Puerto Rico; colony sporulating on oatmeal agar, sporodochia with setae, conidiogenous cells and conidia. Scale bars = 10 µm.

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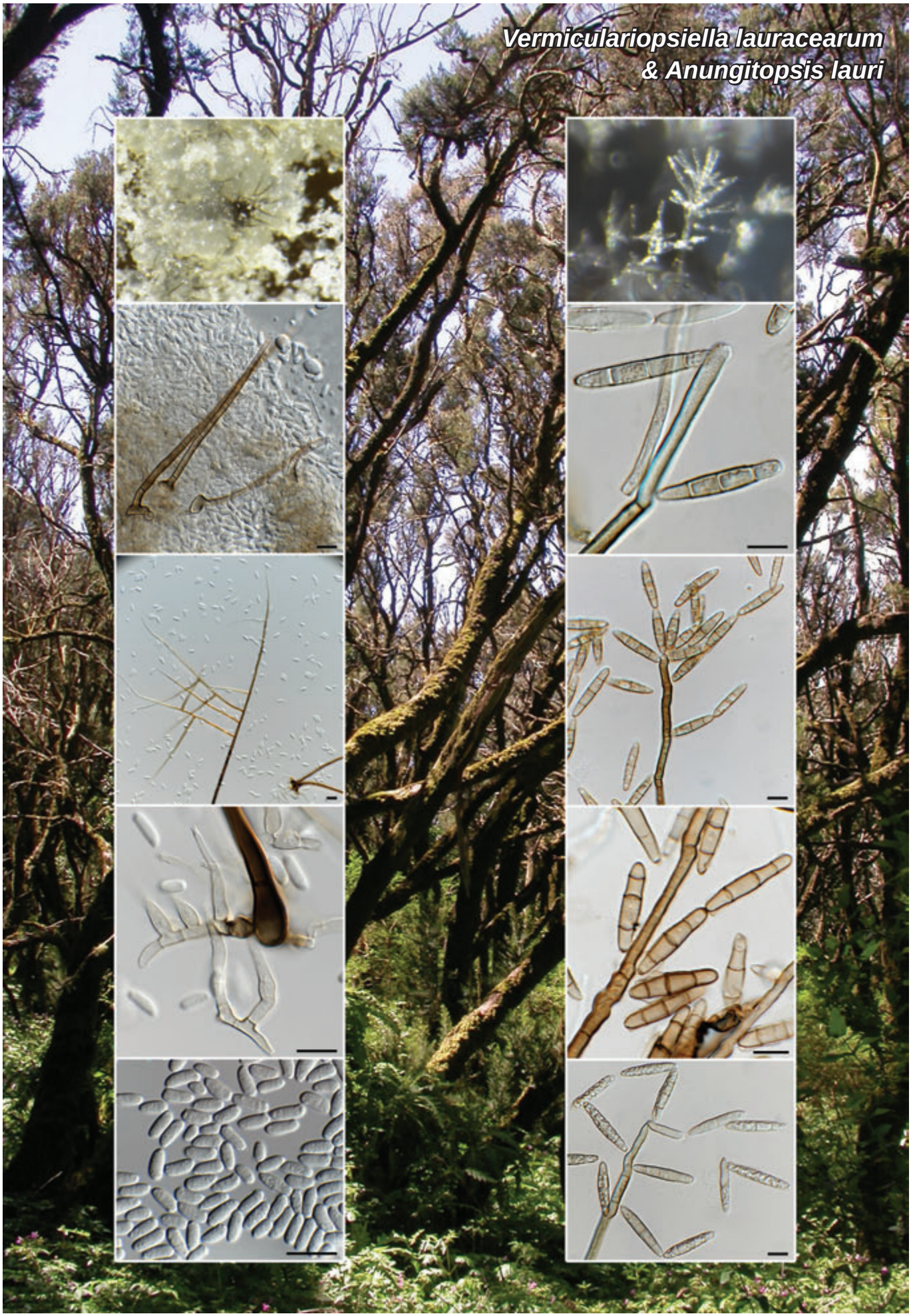
Vermiculariopsiella lauracearum
& Anungitopsis lauri

Fungal Planet 799 & 800 – 14 December 2018

Vermiculariopsiella lauracearum Crous, *sp. nov.*

Etymology. Name refers to *Laurus*, the host genus from which this fungus was isolated.

Classification — *Vermiculariopsiellaceae*, *Vermiculariopsiellales*, *Sordariomycetes*.

Sporodochia developing on OA and PDA, erumpent, crystalline, up to 450 µm diam, with brown, erect setae dispersed throughout sporodochium, thick-walled, smooth-walled, straight to flexuous, 100–300 × 4–5 µm, 8–20-septate, tapering to an obtuse apex and with bulbous base, 7–9 µm diam, forming a series of lateral branches (up to 100 µm long) that again branch once with tertiary branch (up to 120 µm long). *Conidiogenous cells* phialidic, developing in a cluster around the base of setae, pale brown, smooth, subcylindrical with apical taper with periclinal thickening and minute collarette, 1–2 µm long, 20–25 × 3–3.5 µm. *Conidia* aseptate, solitary, hyaline, guttulate, straight to slightly curved, inequilateral with inner plane straight and outer plane convex, apex subobtusely rounded; base truncate but with excentric hilum, 0.5 µm diam, on inner straight plane, (9–)10(–11) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, folded surface, and even, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey, reverse mouse grey. On PDA surface sepia, reverse brown vinaceous. On OA surface mouse grey.

Typus. Spain, La Gomera, leaf litter of *Laurus novocanariensis* (*Lauraceae*), 30 Mar. 2017, *A.L. van Iperen*, HPC 2058 (holotype CBS H-23755, culture ex-type CPC 33591 = CBS 145055, ITS and LSU sequences GenBank MK047436.1 and MK047487.1, MycoBank MB828182).

Notes — Species of *Vermiculariopsiella* produce sporodochia with brown, erect setae, stromatic, sub-hyaline conidiophores, phialidic conidiogenous cells, and hyaline, aseptate conidia (Crous et al. 2014a). There are presently more than 16 species known in the genus. *Vermiculariopsiella lauracearum* is morphologically distinct from known species based on its long, branched setae, and small conidia. *Vermiculariopsis circinotricha*, an apparent coelomycete (*Chaetomella* complex), was described from leaves of *Laurus* '*canariensis*' collected in Madeira (branched setae, conidia cylindrical, 14–19 × 1–1.5 µm). However, Sutton & Sarbhoy (1976) could not locate any type material, and hence the taxonomy of the genus has remained unresolved. Based on the original description and current information about the sexual morph of *Vermiculariopsiella*, it could well be that the illustrated black, ellipsoid sporocarp was of an ascoma (e.g., see *V. dichapetali*), in which case *Vermiculariopsis* would represent an older name for the genus *Vermiculariopsiella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Vermiculariopsiella microsperma* (GenBank KY853478.1; Identities = 530/546 (97 %), 7 gaps (1 %)), *Vermiculariopsiella pediculata* (GenBank MH866028.1; Identities = 530/556 (95 %), 11 gaps (1 %)) and *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 514/540 (95 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Vermiculariopsiella eucalypti* (GenBank KX228303.1; Identities = 815/827 (99 %), no gaps), *Vermiculariopsiella pediculata* (GenBank MH877476.1; Identities = 829/843 (98 %), 3 gaps (0 %)) and *Vermiculariopsiella dichapetali* (GenBank MH107970.1; Identities = 811/839 (97 %), 4 gaps (0 %)).

Anungitopsis lauri Crous, *sp. nov.*

Etymology. Name refers to *Laurus*, the host genus from which this fungus was isolated.

Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes.*

Mycelium consisting of branched, septate, pale olivaceous, smooth, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth-walled, flexuous, arising from superficial hyphae, subcylindrical, rarely branched, multiseptate, 200–500 × 5–6 µm, with basal cell extending from hyphae or globose, up to 8 µm diam, lacking rhizoids. *Conidiogenous cells* integrated, subcylindrical, medium brown, smooth-walled, terminal and intercalary, 20–40 × 4–5 µm, polyblastic, with flat-tipped loci, 2–2.5 µm diam, not thickened nor darkened. *Conidia* in branched chains, subcylindrical to narrowly fusoid with obtusely rounded ends, hila truncate, 1–1.5 µm diam, unthickened, nor darkened, 3(–7)-septate, finely roughened, medina cells medium brown, end cells pale brown, (23–)30–35(–47) × (4–)5 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface olivaceous grey with diffuse peach pigment.

Typus. Spain, La Gomera, leaf litter of *Laurus novocanariensis* (*Lauraceae*), 1300 m altitude, 30 Mar. 2017, *A.L. van Iperen*, HPC 2058 (holotype CBS H-23764, culture ex-type CPC 33999 = CBS 145067, ITS sequence GenBank MK047437.1, MycoBank MB828183).

Notes — *Anungitea* is a genus of hyphomycetes defined as having dark, solitary conidiophores, with a denticulate head with flattened conidiogenous scars that are unthickened and not darkened, and chains of cylindrical, 1-septate subhyaline conidia (Sutton 1973). *Anungitopsis* includes taxa with indistinguishable scars arranged in a rachis, and *Neoanungitea* is intermediate between these two genera, having a rachis, but with flat-tipped loci (Crous et al. 2017b). Crous et al. (2018a) introduced the genus *Pseudoanungitea* for species phylogenetically distinct from *Anungitea* s.str., having terminal and intercalary conidiogenous cells, and refractive, thickened scars that give rise to short conidial chains with somewhat darkened and refractive hila. *Anungitopsis lauri* is phylogenetically distinct from those species presently known from their DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anungitopsis speciosa* (GenBank EU035401.1; Identities = 601/614 (98 %) and *Neoanungitea eucalypti* (GenBank NR_156383.1; Identities = 495/607 (82 %), 41 gaps (6 %)).

Colour illustrations. *Laurus novocanariensis* growing in Spain. Left column, *Vermiculariopsiella lauracearum*, colony on malt extract agar, branched setae, conidiogenous cells and conidia. Right column, *Anungitopsis lauri*, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pararamichloridium caricicola

Fungal Planet 801 – 14 December 2018

Pararamichloridium caricicola Crous, *sp. nov.*

Etymology. Name refers to *Carex*, the host genus from which this fungus was isolated.

Classification — *Pararamichloridiaceae*, *Pararamichloridiales*, *Sordariomycetes.*

Mycelium consisting of brown, smooth, branched, 1.5–2 µm diam hyphae. *Conidiophores* arising from superficial hyphae, subcylindrical, erect, flexuous, unbranched, brown, smooth, 1–6-septate, 35–100 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical with slight apical taper, brown, smooth, 10–25 × 2.5–3 µm; forming a rachis with numerous pimple-like denticles, 0.5 µm diam, inconspicuous, not darkened nor thickened. *Conidia* solitary, aseptate, pale brown, guttulate, covered in a sheath, which gives the surface a wrinkled appearance in lactic acid, ellipsoid, apex obtuse, base truncate, 1.5–2 µm diam, somewhat darkened, (4–)6–7(–8) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse salmon. On PDA surface and reverse greyish with patches of yellow-green. On OA surface buff with patches of ochreous.

Typus. Thailand, Ratchaburi Province, on leaf of *Carex* sp. (*Cyperaceae*), 2008, *P.W. Crous*, HPC 2251 (holotype CBS H-23766, culture ex-type CPC 34533 = CBS 145069, ITS and LSU sequences GenBank MK047438.1 and MK047488.1, MycoBank MB828187).

Notes — *Pararamichloridium* has a ramichloridium-like morphology (Arzanlou et al. 2007), although it clusters distant from *Ramichloridium* s.str. (Videira et al. 2017). The genus presently includes two species (Crous et al. 2017b), that cluster phylogenetically distinct from *P. caricicola.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pararamichloridium verrucosa* (GenBank NR_156653.1; Identities = 502/576 (87 %), 43 gaps (7 %)) and *Pararamichloridium livistonae* (GenBank NR_156652.1; Identities = 533/656 (81 %), 68 gaps (10 %)). Closest hits using the **LSU** sequence are *Pararamichloridium verrucosa* (GenBank MH873621.1; Identities = 882/897 (98 %), no gaps), *Pararamichloridium livistonae* (GenBank NG_058504.1; Identities = 801/836 (96 %), 3 gaps (0 %)) and *Paracapsulospora metroxyli* (as *Sordariomycetidae* sp. SK-2016a, GenBank KX646364.1; Identities = 849/894 (95 %), 5 gaps (0 %)).

Colour illustrations. Indigenous forest in Thailand; colony sporulating on synthetic nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Coniella diospyri

Fungal Planet 802 – 14 December 2018

Coniella diospyri Crous, *sp. nov.*

Etymology. Name refers to *Diospyros*, the host genus from which this fungus was isolated.

Classification — *Schizoparmaceae*, *Diaporthales*, *Sordariomycetes.*

Conidiomata separate, immersed to superficial, hyaline, becoming black, up to 300 µm diam; ostiole central, 20–25 µm diam; conidiomatal wall of 2–6 layers of medium *brown textura angularis*. *Conidiophores* densely aggregated, subulate, frequently branched below, 1–2-septate, 15–25 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, with apical taper, 6–8 × 2.5–3.5 µm, covered in a mucoid sheath, apex with visible periclinal thickening. *Conidia* solitary, aseptate, olivaceous brown, cylindrical, straight, smooth-walled, apex subobtuse, base truncate, multi-guttulate, germ slit absent, (19–)21–23(–25) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse umber. On OA surface dirty white.

Typus. South Africa, Limpopo Province, Kruger National Park, on leaves of *Diospyros mespiliformis* (*Ebenaceae*), 19 Nov. 2010, *P.W. Crous* HPC 2259 (holotype CBS H-23767, culture ex-type CPC 34674 = CBS 145071, ITS, LSU, *rpb2* and *tef1* sequences GenBank MK047439.1, MK047489.1, MK047543.1 and MK047562.1, MycoBank MB828188).

Additional material examined. South Africa, Limpopo Province, Kruger National Park, on leaves of *Trichilia emetica* (*Meliaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2260, specimen CBS H-23786, culture CPC 34676 = CBS 145070, ITS, LSU and *tef1* sequences GenBank MK047440.1, MK047490.1 and MK047563.1.

Notes — The genus *Coniella* was revised by Alvarez et al. (2016), and approximate 30 species are currently accepted in the genus (Marin-Felix et al. 2017, Raudabaugh et al. 2017). *Coniella diospyri* adds an additional species to the genus, being morphologically similar to the *C. castaneicola* complex, although it is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34674 had highest similarity to *Coniella duckerae* (GenBank NR_154851.1; Identities = 600/611 (98 %), 2 gaps (0 %)), *Coniella quercicola* (GenBank AY339345.1; Identities = 562/577 (97 %), 6 gaps (1 %)) and *Coniella limoniformis* (GenBank NR_154819.1; Identities = 549/564 (97 %), 6 gaps (1 %)). The ITS sequences of CPC 34674 and 34676 are identical. Closest hits using the **LSU** sequence of CPC 34674 are *Coniella tibouchinae* (GenBank JQ281776.2; Identities = 900/911 (99 %), 3 gaps (0 %)), *Coniella granati* (GenBank MH869130.1; Identities = 892/901 (99 %), no gaps) and *Coniella straminea* (GenBank MH866234.1; Identities = 890/898 (99 %), 1 gap (0 %)). The LSU sequences of CPC 34674 and 34676 are identical. Closest hits using the ***rpb2*** sequence of CPC 34674 had highest similarity to *Coniella tibouchinae* (GenBank KX833507.1; Identities = 703/767 (92 %), no gaps), *Coniella limoniformis* (GenBank KX833492.1; Identities = 699/767 (91 %), no gaps) and *Coniella africana* (GenBank KX833421.1; Identities = 689/767 (90 %), no gaps). Closest hits using the ***tef1*** sequence of CPC 34674 had highest similarity to *Coniella tibouchinae* (GenBank JQ281778.1; Identities = 348/412 (84 %), 21 gaps (5 %)), *Coniella eucalyptorum* (GenBank KX833634.1; Identities = 292/337 (87 %), 14 gaps (4 %)) and *Coniella africana* (GenBank KX833600.1; Identities = 371/456 (81 %), 28 gaps (6 %)). The *tef1* sequences of CPC 34674 and 34676 are only 93 % (522/564, including 20 gaps) similar.

Colour illustrations. *Diospyros mespiliformis* in Kruger National Park; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pseudorobillarda bolusanthi

Fungal Planet 803 – 14 December 2018

Pseudorobillarda bolusanthi Crous, *sp. nov.*

Etymology. Name refers to *Bolusanthus*, the host genus from which this fungus was isolated.

Classification — *Pseudorobillardaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata immersed, globose, 200–250 µm diam, with central ostiole 50–70 µm diam, surrounded by darker cells than conidiomatal body which is transparent; wall of 3–6 layers of thin-walled, flattened *textura angularis*; conidiomata giving rise to both micro- and macroconidia. *Macroconidiophores* lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth, doliiform, phialidic with periclinal thickening and flared collarette, or proliferating percurrently when older, 4–7(–15) × 3–4 µm. *Paraphyses* numerous, hyphae-like, intermingled among conidiophores, aseptate, flexuous, extending above conidiophores, 50–70 × 1.5–2 µm. *Macroconidia* solitary, (1–)3-septate, guttulate, hyaline, smooth, septa thick and prominent with a central pore linking each cell, apex subobtuse, tapering to a truncate base, 3 µm diam, (21–)26–28(–30) × 6(–7) µm; apical appendages arising from splitting of the conidial sheath, hair-like, flexuous, unbranched, 3–5, up to 30 µm long, fragile, flexuous, unbranched, mostly absent. *Microconidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, proliferating percurrently, 10–15 × 4–5 µm. *Microconidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate, 4–8 × 2–4 µm; apical appendages hair-like, flexuous, unbranched, 3–5, up to 10 µm long, fragile, flexuous, unbranched.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse ochreous. On PDA surface saffron, reverse umber. On OA surface saffron.

Typus. South Africa, Limpopo Province, Kruger National Park, on leaves of *Bolusanthus speciosus* (*Fabaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2263 (holotype CBS H-23782, culture ex-type CPC 34670 = CBS 145072, ITS and LSU sequences GenBank MK047441.1 and MK047491.1, MycoBank MB828189).

Notes — *Pseudorobillarda* was treated by Nag Raj (1993), and presently contains 15 species. Species of *Pseudorobillarda* have been recorded as saprobes, plant pathogens, and endophytes (Vujanovic & St-Arnaud 2003), but have also been isolated from soil (Kadowaki et al. 2014). *Pseudorobillarda bolusanthi* has paraphyses and 3-septate conidia, being most similar to *P. indica* (conidia 14.5–21.5 × 3.5–5.5 µm; Nag Raj 1993), but is distinct in having larger conidia with thick septa, and characteristic microconidia that also bear apical appendages.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudorobillarda siamensis* (GenBank FJ825370.1; Identities = 725/912 (79 %), 56 gaps (6 %)), *Acrocalymma aquatica* (GenBank JX276951.1; Identities = 562/642 (88 %), 20 gaps (3 %)) and *Rhizopycnis vagum* (GenBank HE585021.1; Identities = 558/637 (88 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Pseudorobillarda texana* (GenBank FJ825377.1; Identities = 815/854 (95 %), 4 gaps (0 %)), *Pseudorobillarda sojae* (GenBank KF827458.1; Identities = 814/861 (95 %), 6 gaps (0 %)) and *Pseudorobillarda phragmitis* (GenBank MH869670.1; Identities = 805/859 (94 %), 4 gaps (0 %)).

Colour illustrations. *Bolusanthus speciosus* in Kruger National Park; conidiomata on synthetic nutrient poor agar, conidiogenous cells, paraphyses and conidia. Scale bars: conidiomata = 200 µm, all others = 10 µm.

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Neomyrmecridium septatum

Fungal Planet 804 – 14 December 2018

Neomyrmecridium Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Myrmecridium*.

Classification — *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetes.*

Mycelium consisting of septate, branched hyphae, hyaline, smooth. *Conidiophores* solitary, erect, straight, unbranched, medium brown, smooth, subcylindrical, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, with several denticles at apex; not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, becoming pale brown with age, upper two thirds encased in mucoid sheath, fusoid-ellipsoid, septate.

Type species. *Neomyrmecridium septatum* Crous.
MycoBank MB828190.

Neomyrmecridium septatum Crous, *sp. nov.*

Etymology. Name refers to its septate conidia.

Mycelium consisting of septate, branched hyphae, hyaline, smooth, 2–3 µm diam. *Conidiophores* solitary, erect, straight, unbranched, medium brown, smooth, subcylindrical, 1–4-septate, 40–70 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 30–40 × 4–5 µm, with several denticles at apex, 1–1.5 × 1 µm; not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, becoming pale brown with age, upper two thirds encased in mucoid sheath, 1–2 µm diam, fusoid-ellipsoid, apex obtuse, tapering in lower third to a truncate hilum, 0.5–1 µm diam, (1–)3-septate, (12–)14–16(–20) × (3.5–)4(–5) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface and reverse apricot. On PDA surface apricot, reverse luteous. On OA surface pale luteous.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23768, culture ex-type CPC 34585 = CBS 145073, ITS, LSU, *rpb1*, *rpb2* and *tef1* sequences GenBank MK047442.1, MK047492.1, MK047531.1, MK047544.1 and MK047564.1, MycoBank MB828191).

Notes — *Myrmecridium* is a ramichloridium-like genus with hyaline mycelium, and relatively unpigmented, pimple-like denticles (Arzanlou et al. 2007). The genus presently contains 12 species, all of which are known from their DNA. Species are distinguished based on conidium and conidiophore morphology, as well as DNA phylogeny (Crous et al. 2015a, 2016a).

Myrmecridium sorbicola was recently introduced by Crous et al. (2018a), who commented on the fact that it was distinct from known species of *Myrmecridium* in having septate conidia. In the present additional species are added (also with septate conidia), resolving this clade to represent a new genus, clustering sister to *Myrmecridium* s.str.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myrmecridium sorbicola* (GenBank MH107901.1; Identities = 502/564 (89 %), 19 gaps (3 %)), *Myrmecridium banksiae* (GenBank NR_111762.1; Identities = 480/553 (87 %), 15 gaps (2 %)) and *Myrmecridium spartii* (GenBank KX306762.1; Identities = 483/558 (87 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Myrmecridium sorbicola* (GenBank MH107948.1; Identities = 815/842 (97 %), 2 gaps (0 %)), *Myrmecridium schulzeri* (GenBank MH473005.1; Identities = 857/898 (95 %), 2 gaps (0 %)) and *Pleurophragmium acutum* (GenBank MH876650.1; Identities = 853/894 (95 %), no gaps). No significant hits were obtained when the ***rpb1***, ***rpb2*** and ***tef1*** sequences were used in blastn and megablast searches.

Neomyrmecridium sorbicola (Crous & R.K. Schumach.) Crous, *comb. nov*.

MycoBank MB828192.

Basionym. Myrmecridium sorbicola Crous & R.K. Schumach., Fungal Syst. Evol. 1: 191. 2018.

Colour illustrations. Indigenous forest in Thailand; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Xenodactylaria thailandica

Fungal Planet 805 – 14 December 2018

Xenodactylariaceae Crous, *fam. nov.*

MycoBank MB828248.

Xenodactylaria Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Dactylaria*.

Classification — *Xenodactylariaceae*, *Myrmecridiales*, *Sordariomycetes.*

Mycelium consisting of smooth, hyaline, branched, septate, hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect to flexuous, hyaline, smooth, with 1 to several denticulate apical loci. *Conidia* occurring in branched chains, hyaline, smooth, subcylindrical, septate.

Type species. Xenodactylaria thailandica Crous.
MycoBank MB828193.

Xenodactylaria thailandica Crous, *sp. nov.*

Etymology. Name refers to Thailand, the country where this fungus was collected.

Mycelium consisting of smooth, hyaline, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect to flexuous, 5–20 × 2–3.5 µm, hyaline, smooth, with 1 to several denticulate apical loci, 1–2 × 1.5–2 µm. *Conidia* occurring in branched chains (mostly unbranched), hyaline, smooth, guttulate, subcylindrical, straight, apex obtuse, base truncate, 1.5–2 µm diam, 3(–5)-septate, (20–)24–27(–32) × (3–)4 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey, reverse olivaceous grey in centre, buff in outer region. On PDA surface and reverse buff. On OA surface olivaceous grey.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23769, culture ex-type CPC 34588 = CBS 145074, ITS and LSU sequences GenBank MK047443.1 and MK047493.1, MycoBank MB828194).

Notes — *Dactylaria* (De Hoog 1985) is heterogeneous (Crous et al. 2016a, 2017b), with its type species, *D. purpurella*, clustering in *Magnaporthales* (Klaubauf et al. 2014). *Xenodactylaria* is reminiscent of *Dactylaria* and *Cylindrosympodium*, but distinct in that all structures are hyaline, and conidia occur in short chains. Phylogenetically, it also clusters on its own, and a new genus and family is introduced to accommodate it.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusarium robustum* (GenBank MH861018.1; Identities = 454/548 (83 %), 37 gaps (6 %)), *Fusarium venenatum* (GenBank NR_156290.1; Identities = 454/550 (83 %), 38 gaps (6 %)) and *Fusarium sambucinum* (GenBank KM231813.1; Identities = 451/547 (82 %), 37 gaps (6 %)). Closest hits using the **LSU** sequence are *Acremonium pteridii* (GenBank MH871174.1; Identities = 827/896 (92 %), 9 gaps (1 %)), *Ijuhya dentifera* (GenBank MH872777.1; Identities = 822/892 (92 %), 9 gaps (1 %)) and *Purpureocillium lilacinum* (GenBank MH876802.1; Identities = 826/897 (92 %), 8 gaps (0 %)).

Colour illustrations. Indigenous forest in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.

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Neomyrmecridium asiaticum

Fungal Planet 806 – 14 December 2018

Neomyrmecridium asiaticum Crous, *sp. nov.*

Etymology. Name refers to Asia, the continent where this fungus was collected.

Classification — *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetes.*

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* arising from hyphal coils on creeping hyphae, solitary or in groups of up to three, medium brown, smooth- and thick-walled, mostly unbranched, 2–5-septate, 50–100 × 3–5 µm. *Conidiogenous cells* integrated, terminal, 5–35 × 4–7 µm, subcylindrical, apex obtuse, covered in protruding denticles, 0.5–1 × 1 µm, slightly darkened. *Conidia* solitary, (2–)3-septate, pale brown, thin- and smooth-walled, guttulate, surrounded by a wing-like gelatinous sheath c. 0.5 µm thick, ellipsoid to obovoid, (13–)15–16(–17) × (4–)4.5(–5) µm, tapering in lower conical cell to truncate hilum, 1–1.5 µm diam, not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface luteous with patches of orange, reverse amber. On OA surface luteous with diffuse amber pigment.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23774, culture ex-type CPC 34535 = CBS 145080, ITS and LSU sequences GenBank MK047444.1 and MK047494.1, MycoBank MB828195).

Notes — *Neomyrmecridium asiaticum* represents a new species isolated from dead vines in Thailand, where it co-occurred with another new species, *N. septatum*. *Neomyrmecridium septatum* (conidia (1–)3-septate, (12–)14–16(–20) × (3.5–)4(–5) µm) is similar to *N. asiaticum* based on its conidium morphology, but the two species are phylogenetically distinct. The ITS sequences of *N. septatum* and *N. asiaticum* are 89 % (501/560 including 14 gaps) similar.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neomyrmecridium sorbicola* (GenBank MH107901.1; Identities = 510/562 (91 %), 11 gaps (1 %)), *Myrmecridium phragmitis* (GenBank NR_137782.1; Identities = 489/558 (88 %), 13 gaps (2 %)) and *Ramichloridium schulzeri* (GenBank MH859088.1; Identities = 481/552 (87 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Myrmecridium sorbicola* (GenBank MH107948.1; Identities = 826/842 (98 %), 2 gaps (0 %)), *Myrmecridium schulzeri* (GenBank MH473005.1; Identities = 856/887 (97 %), 2 gaps (0 %)) and *Pleurophragmium acutum* (GenBank MH876650.1; Identities = 853/886 (96 %), no gaps).

Colour illustrations. Agricultural farm in Thailand; colony sporulating on nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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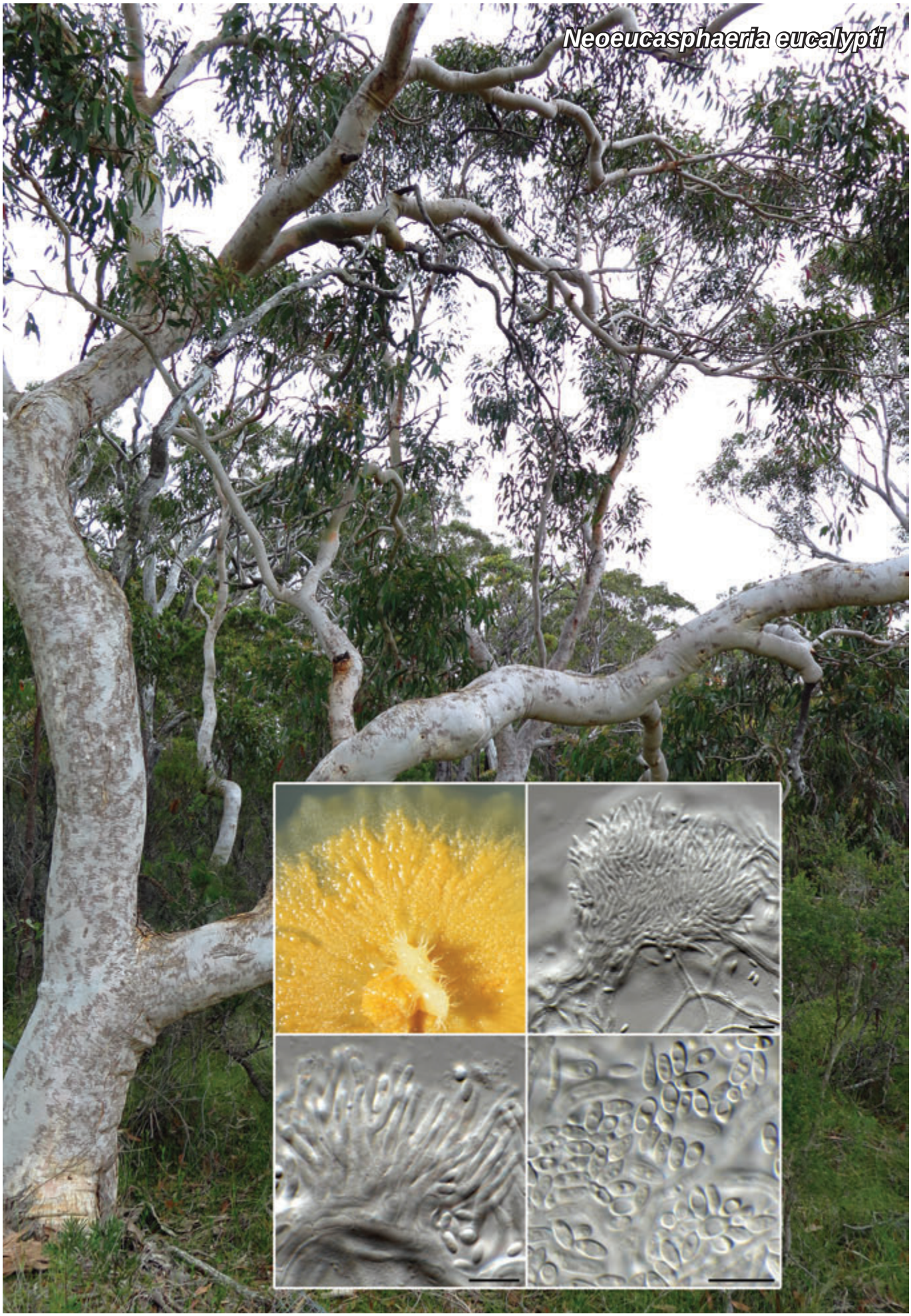
Neoeucasphaeria eucalypti

Fungal Planet 807 – 14 December 2018

Neoeucasphaeria Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Eucasphaeria*.

Classification — *Niessliaceae*, *Hypocreales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, thick-walled, branched, septate, hyphae, frequently encased in mucoid sheath. *Conidiomata* sporodochial, becoming aggregated with age, consisting of a dense series of branches that each give rise to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, phialidic, flexuous, with visible periclinal thickening. *Conidia* aggregating in an orange mass, individually hyaline, smooth, guttulate, ellipsoid, aseptate, straight, apex subobtuse, base truncate.

Type species. *Neoeucasphaeria eucalypti* Crous.
MycoBank MB828249.

Neoeucasphaeria eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Mycelium consisting of hyaline, smooth, thick-walled, branched, septate, 2–4 µm diam hyphae, frequently encased in mucoid sheath. *Conidiomata* sporodochial, 30–100 µm diam, becoming aggregated with age, consisting of a dense series of branches that each give rise to 1–6 conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, phialidic, flexuous, 8–15 × 2–2.5 µm, with visible periclinal thickening. *Conidia* aggregating in an orange mass, individually hyaline, smooth, guttulate, ellipsoid, aseptate, straight, apex subobtuse, base truncate, (3–)4(–5) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, lacking aerial mycelium and smooth (MEA, OA), to feathery (PDA) margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA, surface and reverse orange.

Typus. Australia, Victoria, Arthurs Seat, on *Eucalyptus* sp. (*Myrtaceae*), 23 Dec. 2016, *A.J. Carnegie*, HPC 1938 (holotype CBS H-23770, culture ex-type CPC 33366 = CBS 145075, ITS and LSU sequences GenBank MK047445.1 and MK047495.1, MycoBank MB828196).

Notes — *Neoeucasphaeria eucalypti* clusters basal to *Eucasphaeria* s.str., and is also distinct in having aseptate, ellipsoid conidia. *Eucasphaeria* contains two species, characterised by producing sporodochial conidiomata, hyaline, branched conidiophores, phialidic conidiogenous cells, and hyaline, 0–2-septate, falcate conidia (Crous et al. 2016a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Eucasphaeria rustici* (GenBank KY173410.1; Identities = 534/542 (99 %), 2 gaps (0 %)), *Eucasphaeria capensis* (GenBank NR_156204.1; Identities = 556/565 (98 %), 5 gaps (0 %)) and *Rosasphaeria moravica* (GenBank NR_138377.1; Identities = 545/566 (96 %), 9 gaps (1 %)). Closest hits using the **LSU** sequence are *Eucasphaeria rustici* (GenBank KY173501.1; Identities = 812/819 (99 %), 2 gaps (0 %)), *Eucasphaeria capensis* (GenBank MH874625.1; Identities = 835/844 (99 %), 2 gaps (0 %)) and *Rosasphaeria moravica* (GenBank JF440985.1; Identities = 832/844 (99 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus* forest in Australia; colony sporulating on synthetic nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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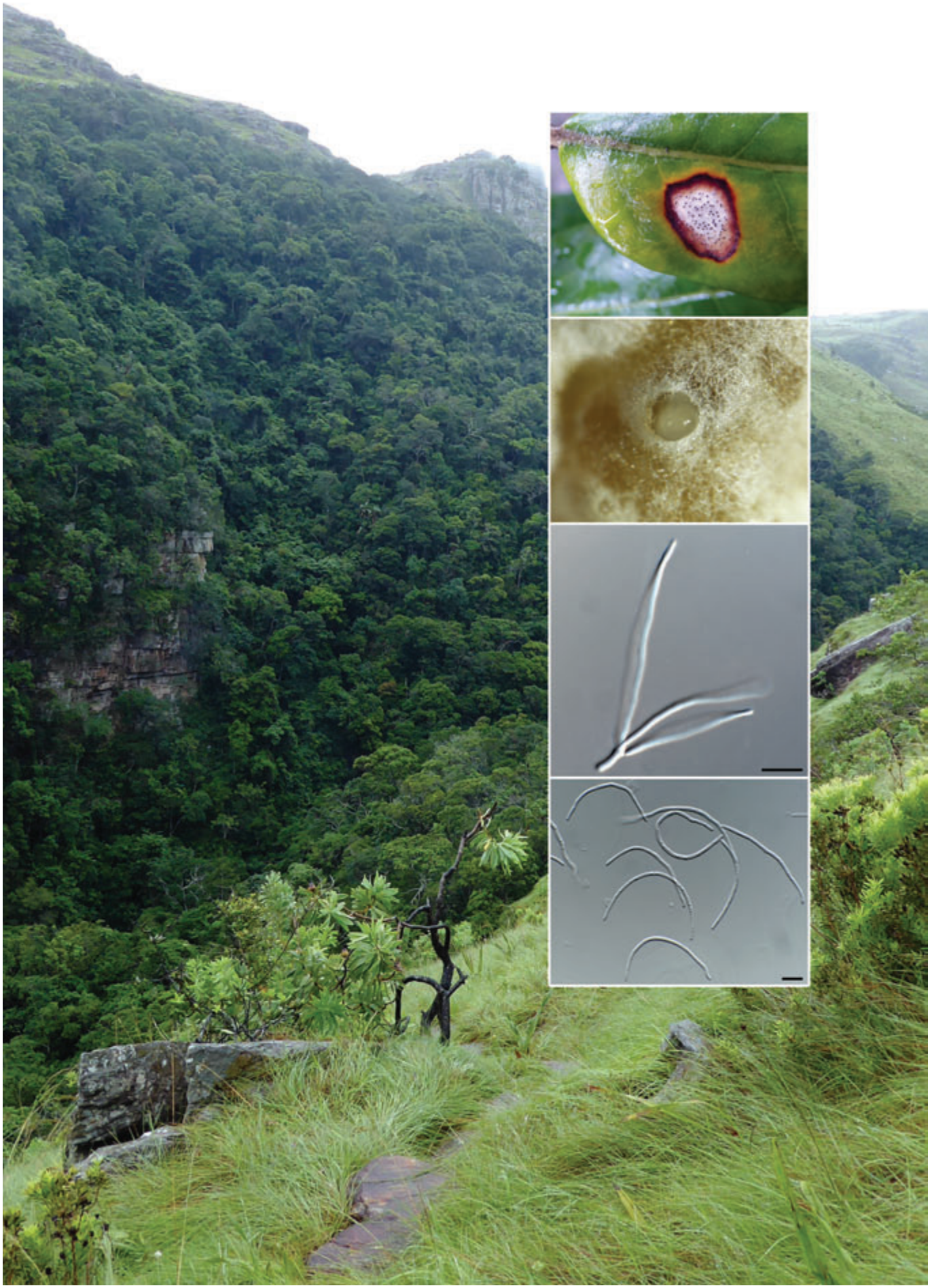
Polyphialoseptoria natalensis

Fungal Planet 808 – 14 December 2018

Polyphialoseptoria natalensis Crous, *sp. nov.*

Etymology. Name refers to the KwaZulu-Natal Province in South Africa, where this fungus was collected.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

Conidiomata brown, erumpent, acervular on OA, globose, 200–350 µm diam; wall of several layers of pale *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, proliferating sympodially at apex, 10–15 × 2.5–3.5 µm, polyphialidic. *Conidia* hyaline, smooth, guttulate, solitary, scolecosporous, irregularly curved, apex subobtuse, base truncate, 3–8-septate, (40–)65–70(–80) × 2(–3) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse luteous. On PDA surface dirty white, reverse umber. On OA surface saffron.

Typus. South Africa, KwaZulu-Natal, Port Edward, Umtamuma N.R., on leaves of unidentified plant host, Feb. 2010, *J. Roux*, HPC 1702 (holotype CBS H-23771, culture ex-type CPC 33214 = CBS 145076, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MK047446.1, MK047496.1, MK047545.1, MK047565.1 and MK047581.1, MycoBank MB828197).

Notes — *Polyphialoseptoria* was established by Quaedvlieg et al. (2013) to accommodate septoria-like species with pycnidial conidiomata, and conidiogenous cells with sympodial, and polyphialidic proliferation. *Polyphialoseptoria natalensis* adds a third species to the genus, which is phylogenetically distinct from the other known taxa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Polyphialoseptoria terminaliae* (GenBank NR_156559.1; Identities = 509/532 (96 %), 9 gaps (1 %)), *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank NR_156558.1; Identities = 490/518 (95 %), 9 gaps (1 %)) and *Xenomycosphaerella diplazii* (GenBank NR_154505.1; Identities = 476/538 (88 %), 29 gaps (5 %)). Closest hits using the **LSU** sequence are *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank KF251716.1; Identities = 810/821 (99 %), no gaps), *Polyphialoseptoria terminaliae* (GenBank MH878128.1; Identities = 820/838 (98 %), 5 gaps (0 %)) and *Hyalozasmidium aerohyalinosporum* (GenBank NG_059440.1; Identities = 811/836 (97 %), 2 gaps (0 %)). Closest hits using the ***rpb2*** sequence are *Polyphialoseptoria terminaliae* (GenBank MF951615.1; Identities = 664/736 (90 %), no gaps), *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank MF951613.1; Identities = 593/666 (89 %), no gaps) and *Deightonomyces daleae* (GenBank MF951485.1; Identities = 520/686 (76 %), 22 gaps (3 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Only distant hits with species of *Mycosphaerellaceae* were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. Forest in Port Edward, Umtamuma, South Africa; symptomatic leaf, colony sporulating on oatmeal agar, conidiogenous cell and conidia. Scale bars = 10 µm.

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Fumagopsis stellae

Fungal Planet 809 – 14 December 2018

Fumagopsis stellae Crous & Carnegie, *sp. nov.*

Etymology. A fungus with star-shaped conidia, named for Stella Carnegie, the star of the Carnegie family.

Classification — *Chaetothyriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Conidiomata sporodochial, slimy, solitary, erumpent, 100–200 µm diam, with dark brown, erect, flexuous, aseptate setae that are thick-walled, up to 90 µm long, 3–5 µm diam. *Mycelium* consisting of pale brown, smooth, septate, branched hyphae, prominently constricted at septa, 2–3.5 µm diam, with several cells becoming swollen and ellipsoid, 4–7 µm diam. *Conidiogenous cells* integrated on hyphae, terminal and lateral, subcylindrical, hyaline, smooth, 8–20 × 3–3.5 µm, mono- to polyblastic. *Conidia* variable, solitary, hyaline, smooth-walled, star-shaped, with 3–4 upright arms and one basal arm attached to the conidiogenous cell; lateral arms 1–3-septate, constricted at septa, ends obtusely rounded, arms 20–40 × 3–5 µm; basal arm 0(–1)-septate, subcylindrical, 10–30 × 3–5 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus. Australia, New South Wales, Kangaroo River State Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 23 Jan. 2010, *A.J. Carnegie*, HPC 1941 (holotype CBS H-23772, culture ex-type CPC 33216 = CBS 145078, ITS and LSU sequences GenBank MK047447.1 and MK047497.1, MycoBank MB828198).

Notes — When this fungus was initially observed on host material, it had sporodochia with brown setae, giving rise to star-shaped conidia. In culture, it formed sporodochia, but very few brown setae were observed. Morphologically, it is reminiscent of *Vonarxia*, having sporodochia with dispersed brown setae, and star-shaped conidia (Crous et al. 2009), but it is phylogenetically distinct, and based on its aseptate setae, we choose to place it in *Fumagopsis*, a genus presently known from two species, *F. complexa* (on *Eugenia jambolana*, India; conidial lateral arms 55–70 × 2–2.8 µm; Wu & Sutton 1995) and *F. triglifioides* (on *Lucuma neriifolia*, Argentina; conidial lateral arms (12–)20–24 × 2–2.5 µm; Van der Aa & Van Oorschot 1985). Although the three species are distinct based on their conidium morphology, there are presently no molecular data to compare them with *F. stellatae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetothyrium brischoficola* (GenBank NR_132849.1; Identities = 523/575 (91 %), 28 gaps (4 %)), *Exophiala eucalyptorum* (GenBank MH863133.1; Identities = 508/573 (89 %), 22 gaps (3 %)) and *Cladophialophora modesta* (GenBank MG757349.1; Identities = 343/388 (88 %), 12 gaps (3 %)). Closest hits using the **LSU** sequence are *Exophiala eucalyptorum* (GenBank KC455258.1; Identities = 821/862 (95 %), 4 gaps (0 %)), *Aphanophora eugeniae* (GenBank NG_056965.1; Identities = 819/862 (95 %), 2 gaps (0 %)) and *Ceramothyrium linnaeae* (GenBank MH874144.1; Identities = 816/861 (95 %), 1 gap (0 %)).

Colour illustrations. *Eucalyptus* forest in Australia; star-shaped conidia, and brown, unbranched seta. Scale bars = 10 µm.

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Cymostachys thailandica

Fungal Planet 810 – 14 December 2018

Cymostachys thailandica Crous, *sp. nov.*

Etymology. Name refers to Thailand, the country where this fungus was collected.

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiophores macronematous, mononematous, mostly in clusters, thin-walled, cymosely branched, erect, straight to flexuous, hyaline, 1–2-septate, smooth to slightly verruculose, 50–120 × 4–5 µm, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* phialidic, clavate, olivaceous brown to dark brown at the apex, paler towards the base, smooth to slightly verruculose, 8–12 × 4–6 µm, with conspicuous collarette. *Conidia* acrogenous, aseptate, fabiform, dark brown, smooth to verruculose, (8–)9(–11) × (4–)5(–6) µm, rounded at ends, aggregating in mucoid mass.

Culture characteristics — Colonies spreading, with folded surface (MEA), sparse aerial mycelium and smooth, lobate margin, reaching 37 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse sienna. On PDA surface and reverse olivaceous grey. On OA surface isabelline.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23773, culture ex-type CPC 34505 = CBS 145079, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MK047448.1, MK047498.1, MK047546.1, MK047566.1 and MK047582.1, MycoBank MB 828199).

Notes — *Cymostachys* was established for stachybotrys-like fungi characterised by irregularly cymosely, branched conidiophores and olivaceous brown to dark brown, fabiform conidia. *Cymostachys thailandica* is phylogenetically distinct, but related to *C. coffeicola*, which is known from leaves of *Coffea arabica* (Cuba), and *Poinsettia* sp. (Thailand) (Lombard et al. 2016). The genus presently includes four species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846052.1; Identities = 562/569 (99 %), 5 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846054.1; Identities = 541/548 (99 %), 5 gaps (0 %)) and *Stachybotrys renispora* (GenBank KU144929.1; Identities = 543/551 (99 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Cymostachys coffeicola* (GenBank MH872746.1; Identities = 889/895 (99 %), 2 gaps (0 %)), *Stachybotrys nephrospora* (GenBank KP893314.1; Identities = 887/892 (99 %), 1 gap (0 %)) and *Memnoniella echinata* (GenBank MH866746.1; Identities = 877/895 (98 %), 3 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846081.1; Identities = 712/721 (99 %), no gaps), *Cymostachys fabispora* (GenBank KU846082.1; Identities = 695/721 (96 %), no gaps) and *Striatibotrys eucylindrospora* (GenBank KU846975.1; Identities = 650/750 (89 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846097.1; Identities = 455/476 (96 %), 2 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846098.1; Identities = 418/478 (87 %), 11 gaps (2 %)) and *Striatibotrys rhabdospora* (GenBank KU847089.1; Identities = 232/263 (88 %), 5 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846113.1; Identities = 336/343 (98 %), no gaps), *Cymostachys fabispora* (GenBank KU846114.1; Identities = 330/343 (96 %), 3 gaps (0 %)) and *Cymostachys garethjonesii* (GenBank KY124126.1; Identities = 274/286 (96 %), 3 gaps (1 %)).

Colour illustrations. Indigenous forest in Thailand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Fusculina eucalyptorum

Fungal Planet 811 – 14 December 2018

Fusculinaceae Crous, *fam. nov.*

Classification — *Fusculinaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium predominantly internal, but external hyphae brown, thick-walled, giving rise to chlamydospore-like cells. *Conidiomata* pycnidial, immersed, becoming slightly erumpent, brown, opening by irregular rupture; wall consisting of several layers of brown cells of *textura angularis. Paraphyses* intermingled among conidiogenous cells, cylindrical, branched below, septate; at times becoming fertile. *Conidiophores* reduced to dimorphic conidiogenous cells. *Primary conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, proliferating several times percurrently near apex, giving rise to *primary conidia*, hyaline to brown, smooth to verruculose, subcylindrical, obovoid to semiclavate, aseptate or 1-septate, with or without mucoid sheath. *Secondary conidiogenous cells* integrated among primary conidiogenous cells, hyaline, smooth, proliferating sympodially. *Secondary conidia* hyaline, smooth, granular, ellipsoid with rounded ends, or subcylindrical with obtuse apex and truncate base.

Type genus. *Fusculina* Crous & Summerell.
MycoBank MB828200.

Note — The family *Fusculinaceae* presently includes *Fusculina* and *Gordonomyces*. Both genera are associated with leaf spots, occurring on respectively *Myrtaceae* and *Proteaceae*.

Fusculina eucalyptorum Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Conidiomata solitary, erumpent, pycnidial, globose, brown, 200–250 µm diam, exuding a creamy conidial mass; wall of 6–8 layers of brown *textura angularis*. On OA paraphyses observed among conidiophores, hyaline, smooth, septate, hyphae-like, 2–3 µm diam. On OA conidiomata are surrounded by chains of chlamydospore-like cells, prominently constricted at septa, hyaline to brown, 0–1-septate, up to 8 µm diam. *Conidiophores* lining the inner cavity, subcylindrical, 15–25 × 4–5 µm, smooth, hyaline, giving rise to 1–2 conidiogenous cells. *Conidiogenous cells* hyaline, smooth, terminal and intercalary, 7–15 × 3–4 µm, proliferating percurrently. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, fusoid, apex subobtuse, base truncate, 2–2.5 µm diam, (10–)13–15(–17) × (3.5–)4 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff to isabelline.

Typus. Australia, New South Wales, Mount Grenfell Historic Site, on leaves of *Eucalyptus socialis* (*Myrtaceae*), 24 Aug. 2015, *B.A. Summerell*, HPC 2221 (holotype CBS H-23775, culture ex-type CPC 34407 = CBS 145083, ITS and LSU sequences GenBank MK047449.1 and MK047499.1, MycoBank MB828201).

Notes — The monotypic genus *Fusculina* was established for a fusicoccum-like genus occurring on leaf spots of *Eucalyptus* (Summerell et al. 2006). *Fusculina eucalyptorum* is distinct from *F. eucalypti* (conidia 16–22 × 3–4 µm) by having smaller conidia, and lacking secondary conidia and chlamydospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusculina eucalypti* (GenBank NR_132812.1; Identities = 653/712 (92 %), 9 gaps (1 %)), *Gordonomyces mucovaginatus* (GenBank NR_157428.1; Identities = 447/501 (89 %), 22 gaps (4 %)) and *Preussia minima* (GenBank JX427054.1; Identities = 380/471 (81 %), 21 gaps (4 %)). Closest hits using the **LSU** sequence are *Fusculina eucalypti* (GenBank DQ923531.1; Identities = 880/888 (99 %), no gaps), *Gordonomyces mucovaginatus* (GenBank NG_057941.1; Identities = 836/863 (97 %), 5 gaps (0 %)) and *Murispora fagicola* (GenBank NG_060797.1; Identities = 824/895 (92 %), 12 gaps (1 %)).

Colour illustrations. Mount Grenfell, Australia; colony sporulating on synthetic nutrient poor agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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Neodevriesia metrosideri

Fungal Planet 812 – 14 December 2018

Neodevriesia metrosideri Crous, *sp. nov.*

Etymology. Name refers to *Metrosideros*, the host genus from which this fungus was isolated.

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, subcylindrical, pale brown, smooth-walled, 1–4-septate, 8–30 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth, 5–8 × 2.5–3 µm; loci inconspicuous, truncate, sympodial, 1–1.5 µm diam, not thickened nor darkened. *Conidia* occurring in branched chains, pale to medium brown, smooth-walled, guttulate, subcylindrical, 1–4-septate; ramoconidia 10–15 × 2–3 µm; conidia (10–)12–15(–17) × 2–3 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. New Zealand, Great Barrier Island, on *Metrosideros* sp. (*Myrtaceae*), 31 Aug. 2017, *R. Thangavel*, T17_03062B (holotype CBS H-23776, culture ex-type CPC 34458 = CBS 145084, ITS and LSU sequences GenBank MK047450.1 and MK047500.1, MycoBank MB828202).

Notes — The genus *Neodevriesia* (Quaedvlieg et al. 2014) which presently includes approximately 20 species, is discussed elsewhere in this paper. *Neodevriesia metrosideri* is phylogenetically distinct from all species in the genus. An interesting aspect of this species is the prominent difference between young and mature conidia, where young conidial chains are slender and pale olivaceous, and older chains are wider, prominently constricted at septa, and darker brown.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 544/558 (97 %), 4 gaps (0 %)), *Devriesia fraserae* (as *Devriesia fraseriae*, GenBank NR_144961.1; Identities = 533/559 (95 %), 9 gaps (1 %)) and *Devriesia sardiniae* (GenBank KP791766.1; Identities = 529/555 (95 %), 4 gaps (1 %)). Closest hits using the **LSU** sequence are *Neodevriesia lagerstroemiae* (GenBank KF902149.1; Identities = 738/746 (99 %), no gaps), *Neodevriesia knoxdaviesii* (as *Teratosphaeria knoxdaviesii*, GenBank EU707865.1; Identities = 831/843 (99 %), 2 gaps (0 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578114.1; Identities = 825/839 (98 %), no gaps).

Colour illustrations. *Metrosideros* sp. growing in New Zealand; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Gnomoniopsis rosae

Fungal Planet 813 – 14 December 2018

Gnomoniopsis rosae Crous, *sp. nov.*

Etymology. Name refers to *Rosa*, the host genus from which this fungus was isolated.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes.*

Conidiomata erumpent, globose, brown, 200–400 µm diam, acervular, opening by irregular rupture, exuding a creamy conidial mass; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, 0–2-septate, subcylindrical, branched at base or not, 10–20 × 3–4 µm. *Conidiogenous cells* integrated, terminal and intercalary, hyaline, smooth, subcylindrical with apical taper, 6–13 × 2.5–3.5 µm; phialidic with prominent periclinal thickening. *Conidia* solitary, aseptate, fusoid, straight, hyaline, smooth-walled, guttulate, apex subobtuse, base truncate, 1 µm diam, (9–)10–12(–13) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface greyish sepia, reverse umber. On OA surface ochreous centre, greyish sepia in outer region.

Typus. New Zealand, Auckland, Auckland Botanical Garden, on *Rosa* sp. (*Rosaceae*), 30 Aug. 2017, *R. Thangavel*, T17-03040A (holotype CBS H-23777, culture ex-type CPC 34440 = CBS 145085, ITS, LSU and *rpb2* sequences GenBank MK047451.1, MK047501.1 and MK047547.1, MycoBank MB828203).

Notes — *Gnomoniopsis* represents a genus of mostly host-specific fungi (Sogonov et al. 2008, Walker et al. 2010). *Gnomoniopsis rosae* is phylogenetically distinct from the species presently known from DNA. Unfortunately, only the asexual morph was found, making comparisons with older literature difficult.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cryptosporella umbrina* (GenBank MH855393.1; Identities = 618/620 (99 %), no gaps), *Discula quercina* (GenBank GQ452265.1; Identities = 574/623 (92 %), 30 gaps (4 %)) and *Gnomoniopsis smithogilvyi* (GenBank KY930638.1; Identities = 572/623 (92 %), 32 gaps (5 %)). Closest hits using the **LSU** sequence are *Gnomoniopsis smithogilvyi* (GenBank MH877030.1; Identities = 898/898 (100 %), no gaps), *Cryptosporella umbrina* (GenBank MH866843.1; Identities = 895/896 (99 %), 1 gap (0 %)) and *Gnomoniopsis idaeicola* (GenBank MH875092.1; Identities = 893/895 (99 %), no gaps). Closest hits using the ***rpb2*** sequence are *Gnomoniopsis paraclavulata* (GenBank EU219248.1; Identities = 692/758 (91 %), no gaps), *Discula campestris* (GenBank EU199143.1; Identities = 692/758 (91 %), no gaps) and *Gnomoniopsis clavulata* (GenBank EU219251.1; Identities = 689/758 (91 %), no gaps).

Colour illustrations. *Rosa* sp. growing in New Zealand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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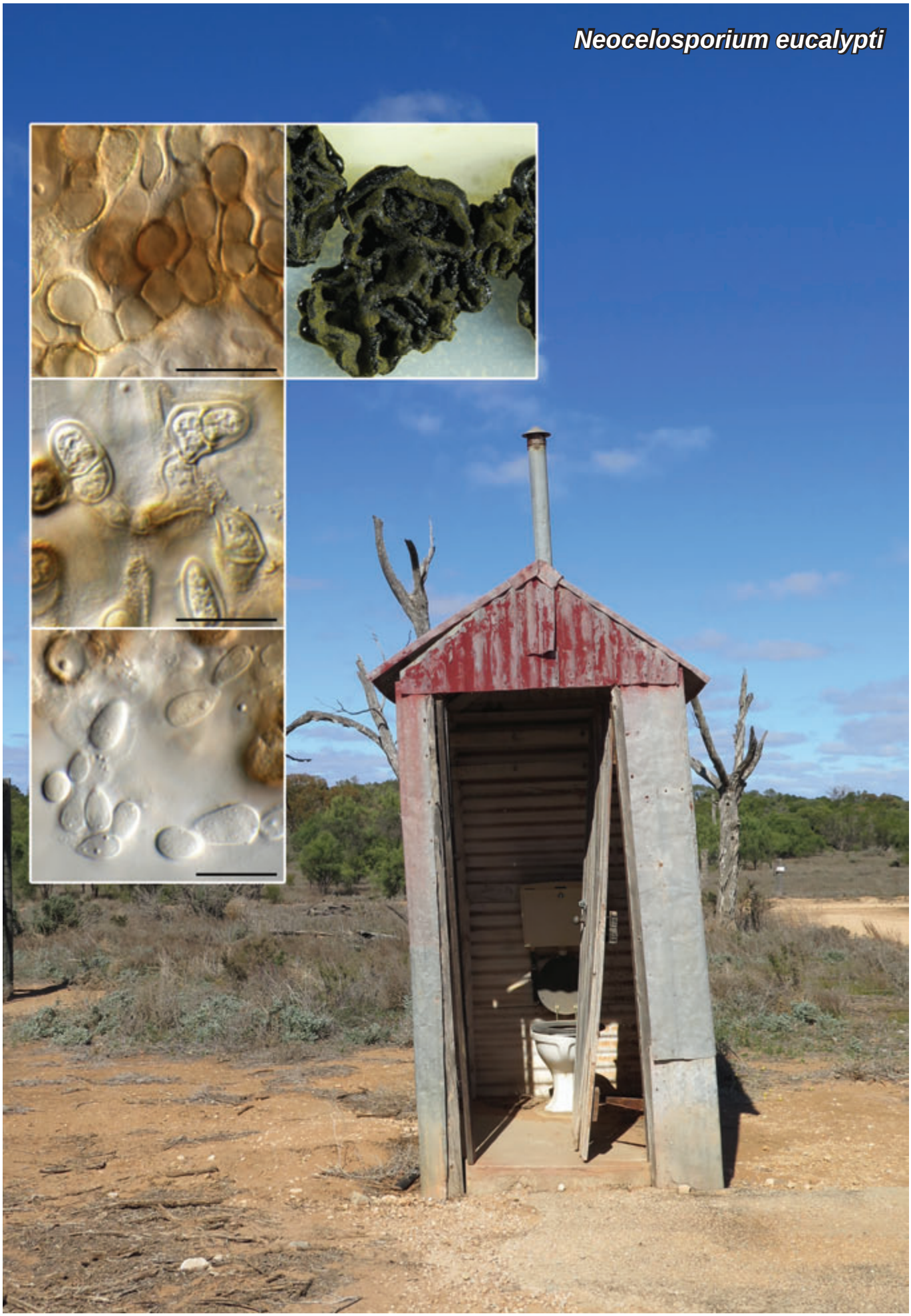
Neocelosporium eucalypti

Fungal Planet 814 – 14 December 2018

Neocelosporiales Crous, *ord. nov*.

MycoBank MB828204.

Neocelosporiaceae Crous, *fam. nov.*

Classification — *Neocelosporiaceae*, *Neocelosporiales*, *Dothideomycetes.*

Mycelium spreading, enclosed in mucus, consisting of medium to dark brown, verruculose hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid, or hyphae forming cellular clumps with endoconidia. *Primary conidia* hyaline to brown, thin- to thick-walled, 0–3-septate, giving rise to *secondary conidia* via microcyclic conidiation. *Ascomata* globose, solitary to gregarious; wall of several layers of brown, thick-walled *textura angularis. Asci* 8-spored, bitunicate, fissitunicate, subcylindrical to clavate with ocular chamber. *Pseudoparaphyses* hyphae-like, anastomosting, branched, septate. *Ascospores* biseriate, ellipsoid to fusoid, brown, 3–4-septate, constricted at septa, smooth-walled, with mucilaginous sheath.

Type genus. *Neocelosporium* Crous.
MycoBank MB828205.

Note — The order *Neocelosporiales* presently includes three genera, *Neocelosporium*, *Celosporium* and *Muellerites*.

Neocelosporium Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Celosporium*.

Mycelium spreading, enclosed in mucus, consisting of medium to dark brown, verruculose, hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid. *Primary conidia* brown, thick-walled, giving rise to *secondary conidia* via microcyclic conidiation, ellipsoid, hyaline, smooth-walled, aseptate, apex obtuse, base truncate, forming on primary conidia or hyphal cells, becoming brown and thick-walled and swollen with age.

Type species. *Neocelosporium eucalypti* Crous.
MycoBank MB828206.

Neocelosporium eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Mycelium spreading, enclosed in mucus, medium to dark brown, verruculose, consisting of 4–5 µm diam hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid, 5–10 µm diam. *Primary conidia* brown, thick-walled, giving rise to *secondary conidia* via microcyclic conidiation, ellipsoid, hyaline, smooth-walled, aseptate, apex obtuse, base truncate, forming on primary conidia or hyphal cells, 5–12 × 3–5 µm, becoming brown and thick-walled and swollen with age.

Culture characteristics — Colonies erumpent, spreading, with folded surface, sparse aerial mycelium and feathery, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse leaden black.

Typus. Australia, New South Wales, Mildura, Mungo National Park, on *Eucalyptus cyanophylla* (*Myrtaceae*), 27 Aug. 2015, *B.A. Summerell*, HPC 2224 (holotype CBS H-23778, culture ex-type CPC 34468 = CBS 145086, ITS and LSU sequences GenBank MK047452.1 and MK047502.1, MycoBank MB828207).

Notes — *Neocelosporium eucalypti* clusters with *Muellerites juniperi* (CBS 339.73) and *Celosporium laricicola* (Tsuneda et al. 2010). *Neocelosporium* is morphologically distinct, in that it has hyaline conidia that primarily arise on the surface of hyphae (clumps with a limited number of large, brown endoconidia are observed), whereas *Celosporium* is characterised by dematiaceous hyphae forming clumps with numerous hyaline to brown endoconidia.

Based on a megablast search of NCBIs GenBank nucleotide database, only distant hits were obtained using the **ITS** sequence, including *Celosporium larixicola* (GenBank FJ997287.1; Identities = 498/544 (92 %), 11 gaps (2 %)), *Gonatobotryum apiculatum* (GenBank MH859103.1; Identities = 531/597 (89 %), 21 gaps (3 %)) and *Scleroconidioma sphagnicola* (GenBank DQ182416.1; Identities = 511/578 (88 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Celosporium larixicola* (GenBank FJ997288.1; Identities = 789/816 (97 %), 2 gaps (0 %)), *Muellerites juniperi* (GenBank MH877745.1; Identities = 817/846 (97 %), 4 gaps (0 %)) and *Dothiora europaea* (GenBank MH872143.1; Identities = 843/883 (95 %), 2 gaps (0 %)).

Colour illustrations. Mildura, Mungo National Park, Australia; brown hyhae constricted at septa, colony on potato dextrose agar, and conidia. Scale bars = 10 µm.

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Rachicladosporium corymbiae

Fungal Planet 815 – 14 December 2018

Rachicladosporium corymbiae Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes.*

Ascomata formed on PNA *in vitro*. *Ascomata* brown, globose, 70–90 µm diam, with central ostiole; wall of 3–4 layers of brown, flattened *textura angularis. Asci* bitunicate, sessile, fasciculate, obovoid with minute ocular chamber, 1–2 µm diam, 20–25 × 7–10 µm. *Pseudoparaphyses* absent. *Ascospores* multiseriate, hyaline, smooth, fusoid-ellipsoid, widest in middle of apical cell, constricted at septum, guttulate, 9–10 × 3 µm. *Mycelium* consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, medium brown, unbranched, smooth to verruculose, 10–30 × 3–4 µm. *Conidiogenous cells* terminal, integrated, brown, finely verruculose, subcylindrical, 10–20 × 3–4 µm; proliferating sympodially with 1–3 apical loci, darkened, thickened, 1.5–2 µm diam. *Conidia* occurring in branched chains, subcylindrical, tapering at both ends, 0–1-septate, verruculose to warty, brown; ramoconidia (9–)10–15 × 2.5–3.5 µm; conidia (8–)9–10(–12) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey. On PDA and OA surface and reverse iron-grey.

Typus. Ghana, on leaf spots of *Corymbia citriodora* (*Myrtaceae*), 21 June 2010, *M.J. Wingfield*, HPC 2172 (holotype CBS H-23779, culture ex-type CPC 34021 = CBS 145087, ITS and LSU sequences GenBank MK047453.1 and MK047503.1, MycoBank MB828208).

Notes — Isolations were made from single germinating ascospores with an irregular mode of germination. Both the sexual and asexual morph formed in culture. *In vivo* ascomata were associated with *Teratosphaeria* spp., co-occurring on leaf spots. *Rachicladosporium* includes species associated with leaf spots that have a cladosporium-like morphology, but distinct in that conidiophores have an apical rachis, and conidia have slightly thickened hila (Crous et al. 2007a). *Rachicladosporium eucalypti* has a sexual mycosphaerella-like morph (Crous et al. 2014b), similar to that of *R. corymbiae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rachicladosporium eucalypti* (GenBank NR_155718.1; Identities = 544/574 (95 %), 6 gaps (1 %)), *Rachicladosporium pini* (GenBank JF951145.1; Identities = 544/574 (95 %), 5 gaps (0 %)) and *Rachicladosporium luculiae* (GenBank MH863123.1; Identities = 539/576 (94 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Rachicladosporium luculiae* (GenBank EU040237.1; Identities = 844/847 (99 %), 2 gaps (0 %)), *Rachicladosporium pini* (GenBank MH876826.1; Identities = 843/847 (99 %), 2 gaps (0 %)) and *Rachicladosporium paucitum* (GenBank KF309988.1; Identities = 759/763 (99 %), 2 gaps (0 %)).

Colour illustrations. Mixed forest in Ghana; symptomatic leaf, ascomata forming on pine needle agar, pseudothecium, asci, conidiophores, conidiogenous cells and conidia. Scale bars: ascoma = 100 µm, all others = 10 µm.

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Neofitzroyomyces nerii

Fungal Planet 816 – 14 December 2018

Neofitzroyomyces Crous, *gen. nov.*

Etymology. Name relfects its morphological similarity to the genus *Fitzroyomyces*.

Classification — *Stictidaceae*, *Ostropales*, *Lecanoromycetes.*

Conidiomata solitary, becoming aggregated, globose, hyaline to subhyaline, eustromatic, pycnidial; ostiole central; wall of several layers of hyaline to subhyaline *textura angularis. Conidiophores* hyaline, lining the inner cavity, subcylindrical, unbranched, septate, each giving rise to a cluster of up to 6 conidiogenous cells. *Conidiogenous cells* subcylindrical, terminal, hyaline, smooth, proliferating sympodially with several flat-tipped apical loci, not thickened nor darkened. *Conidia* solitary, aggregating in mucoid droplet, hyaline, smooth, flexuous, acicular, apex subobtuse, base truncate, septate, septoria-like in appearance.

Type species. *Neofitzroyomyces nerii* Crous.
MycoBank MB828209.

Neofitzroyomyces nerii Crous, *sp. nov.*

Etymology. Name refers to *Nerium*, the host genus from which this fungus was isolated.

Conidiomata solitary, becoming aggregated, globose, hyaline to subhyaline, eustromatic, pycnidial, 80–150 µm diam; ostiole 20–30 µm diam; wall of 5–8 layers of hyaline to subhyaline *textura angularis. Conidiophores* hyaline, lining the inner cavity, subcylindrical, unbranched, 0–1-septate, 5–7 × 2–3 µm, each giving rise to a cluster of up to 6 conidiogenous cells. *Conidiogenous cells* subcylindrical, terminal, hyaline, smooth, 5–10 × 2–3 µm, proliferating sympodially with several flat-tipped apical loci, 0.5–1 µm diam, not thickened nor darkened. *Conidia* solitary, aggregating in mucoid droplet, hyaline, smooth, flexuous, acicular, apex subobtuse, base truncate, 3–6-septate, septoria-like in appearance, (25–)40–65(–80) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA, surface and reverse ochreous.

Typus. France, Mazan, associated with leaf spots on *Nerium oleander* (*Apocynaceae*), 20 July 2017, *P.W. Crous*, HPC 2191 (holotype CBS H-23780, culture ex-type CPC 33883 = CBS 145088, ITS and LSU sequences GenBank MK047454.1 and MK047504.1, MycoBank MB828210).

Notes — *Neofitzroyomyces* is phylogenetically closely related to the monotypic genus *Fitzroyomyces*, which was established for a septoria-like fungus occurring on leaves of *Cyperaceae* in Australia (Crous et al. 2017b). *Neofitzroyomyces* differs from *Fitzroyomyces* in that it has well-defined conidiophores, and conidiogenous cells that proliferate sympodially, with several flat-tipped apical loci.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fitzroyomyces cyperi* (GenBank NR_156387.1; Identities = 419/466 (90 %), 13 gaps (3 %)), *Carestiella socia* (GenBank AY661682.1; Identities = 381/437 (87 %), 22 gaps (5 %)) and *Phacidiella eucalypti* (GenBank MH863073.1; Identities = 465/544 (85 %), 24 gaps (4 %)). Closest hits using the **LSU** sequence are *Phacidiella podocarpi* (GenBank NG_058118.1; Identities = 761/803 (95 %), 5 gaps (0 %)), *Conotrema populorum* (GenBank AY340542.1; Identities = 785/831 (94 %), 7 gaps (0 %)) and *Phacidiella eucalypti* (GenBank EF110617.1; Identities = 781/829 (94 %), 4 gaps (0 %)).

Colour illustrations. *Nerium oleander* with leaf spots in Mazan, France; conidiomata sporulating on potato dextrose agar, section through ascoma showing pale brown wall, conidiogenous cells and conidia. Scale bars: conidioma = 150 µm, all others = 10 µm.

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Corynespora thailandica

Fungal Planet 817 – 14 December 2018

Corynespora thailandica Crous, *sp. nov.*

Etymology. Name refers to Thailand, the country where this fungus was collected.

Classification — *Corynesporascaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of brown, finely roughened, branched, septate, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched, brown, thick-walled, finely roughened, base swollen, up to 12 µm diam, conidiophores extremely long in culture, 5–6 µm diam, multi-septate. *Conidiogenous cells* integrated, terminal, monotretic, subcylindrical, brown, finely roughened, slightly darkened at apex, 3–4 µm diam, 25–30(–60) × 5–6 µm. *Conidia* obclavate, mostly solitary, thick-walled, brown, finely roughened, 4–8-distoseptate, (50–)80–110(–200) × (9–)10–12(–13) µm; hila darkened, thickened, 3–4 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 10 mm diam on PDA, 60 mm diam on OA and MEA after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. Thailand, Nakhon Nayok Province, Wang Takhrai, on wood in forest, 2008, *P.W. Crous*, HPC 2143 (holotype CBS H-23781, culture ex-type CPC 33935 = CBS 145089, ITS, LSU and *tef1* sequences GenBank MK047455.1, MK047505.1 and MK047567.1, MycoBank MB828211).

Notes — The genus *Corynespora* is polyphyletic (Voglmayr & Jaklitsch 2017). Species occur on a range of substrates, varying from leaves to twigs, with several being regarded as serious plant pathogens. Based on the species treated by Ellis (1971, 1976), and those known from DNA sequence data, the present collection appears to represent a new taxon, described here as *Corynespora thailandica*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Corynespora cassiicola* (GenBank FJ852592.1; Identities = 537/557 (96 %), 6 gaps (1 %)), *Corynespora smithii* (GenBank KY984300.1; Identities = 536/558 (96 %), 9 gaps (1 %)) and *Corynespora torulosa* (GenBank NR_145181.1; Identities = 530/556 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Corynespora cassiicola* (GenBank MH869486.1; Identities = 840/847 (99 %), 2 gaps (0 %)), *Corynespora torulosa* (GenBank NG_058866.1; Identities = 839/847 (99 %), 2 gaps (0 %)) and *Corynespora smithii* (GenBank KY984299.1; Identities = 839/847 (99 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Corynespora smithii* (GenBank KY984436.1; Identities = 396/464 (85 %), 19 gaps (4 %)), *Pyrenochaeta nobilis* (GenBank MF795880.1; Identities = 289/348 (83 %), 27 gaps (7 %)) and *Neocucurbitaria acerina* (GenBank MF795856.1; Identities = 286/347 (82 %), 17 gaps (4 %)).

Colour illustrations. Indigenous forest in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.

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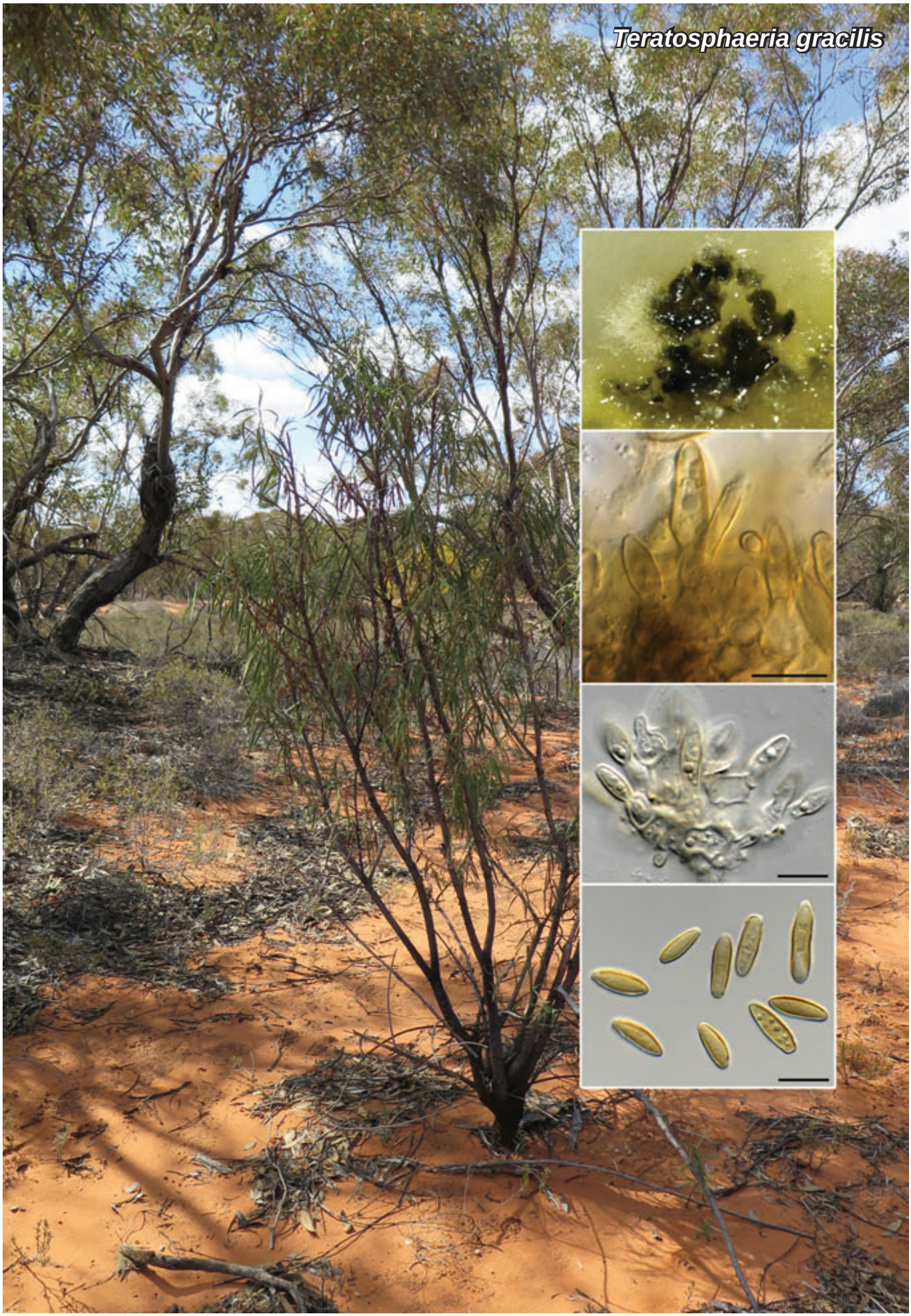
Teratosphaeria gracilis

Fungal Planet 818 – 14 December 2018

Teratosphaeria gracilis Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus gracilis*, the host species from which this fungus was isolated.

Classification — *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes.*

Associated with insect damage on leaves. *Conidiomata* immersed, globose, dark brown, pycnidial, 90–120 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* brown, finely roughened, doliiform, 5–9 × 5–7 µm, proliferating percurrently at apex. *Conidia* solitary, fusoid to subcylindrical, apex subobtuse, base truncate, 2–4 µm diam, with minute marginal frill, 0(–1)-septate, guttulate, brown, finely roughened, (12–)15–20(–25) × (3.5–)4–5(–6) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface grey, reverse olivaceous grey. On PDA surface smoke grey, reverse olivaceous grey. On OA surface isabelline with patches of olivaceous grey.

Typus. Australia, New South Wales, Mildura, Mungo National Park, on *Eucalyptus gracilis* (*Myrtaceae*), 27 Aug. 2015, *B.A. Summerell*, HPC 2225 (holotype CBS H-23783, culture ex-type CPC 34393 = CBS 145090, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047456.1, MK047506.1, MK047523.1, MK047529.1, MK047548.1, MK047568.1 and MK047583.1, MycoBank MB828212).

Notes — Numerous species of *Teratosphaeria* are associated with *Teratosphaeria* leaf disease (TLD) of *Eucalyptus* and the closely related genus *Corymbia* (Hunter et al. 2011). *Teratosphaeria* was recently treated by Quaedvlieg et al. (2014), resulting in the majority of the species occurring on eucalypts now being known from their DNA data. *Teratosphaeria gracilis* appears to represent yet another phylogenetically distinct species in the complex.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria miniata* (GenBank MH863451.1; Identities = 485/501 (97 %), 2 gaps (0 %)), *Teratosphaeria biformis* (GenBank MH863387.1; Identities = 485/501 (97 %), 2 gaps (0 %)) and *Teratosphaeria molleriana* (GenBank MH862864.1; Identities = 485/501 (97 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Teratosphaeria stellenboschiana* (GenBank MH874553.1; Identities = 879/882 (99 %), no gaps), *Teratosphaeria gauchensis* (GenBank EU019290.1; Identities = 871/874 (99 %), 1 gap (0 %)) and *Teratosphaeria zuluensis* (GenBank MH874640.1; Identities = 878/882 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Teratosphaeria destructans* (GenBank KF903447.1; Identities = 506/539 (94 %), 2 gaps (0 %)), *Teratosphaeria viscida* (GenBank KF903563.1; Identities = 505/539 (94 %), 2 gaps (0 %)) and *Teratosphaeria eucalypti* (GenBank KF903452.1; Identities = 505/540 (94 %), 3 gaps (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaeria blakelyi* (GenBank KF902704.1; Identities = 371/411 (90 %), 10 gaps (2 %)), *Teratosphaeria majorizuluensis* (GenBank KF902733.1; Identities = 363/402 (90 %), 8 gaps (1 %)) and *Teratosphaeria gauchensis* (GenBank KF902727.1; Identities = 394/446 (88 %), 18 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 775/868 (89 %), 2 gaps (0 %)), *Teratosphaeria stellenboschiana* (GenBank MF951743.1; Identities = 783/883 (89 %), no gaps) and *Teratosphaeria gauchensis* (GenBank KX348103.1; Identities = 783/883 (89 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria miniata* (GenBank KF903323.1; Identities = 305/357 (85 %), 15 gaps (4 %)), *Teratosphaeria juvenalis* (GenBank KF903318.1; Identities = 307/361 (85 %), 22 gaps (6 %)) and *Teratosphaeria mareebensis* (GenBank KF903320.1; Identities = 302/359 (84 %), 13 gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria destructans* (GenBank KT343568.1; Identities = 517/603 (86 %), 19 gaps (3 %)), *Teratosphaeria nubilosa* (GenBank AY725599.1; Identities = 517/604 (86 %), 24 gaps (3 %)) and *Teratosphaeria zuluensis* (as *Coniothyrium zuluense*, GenBank AY244389.1; Identities = 362/403 (90 %), 12 gaps (2 %)).

Colour illustrations. Mungo National Park, Australia; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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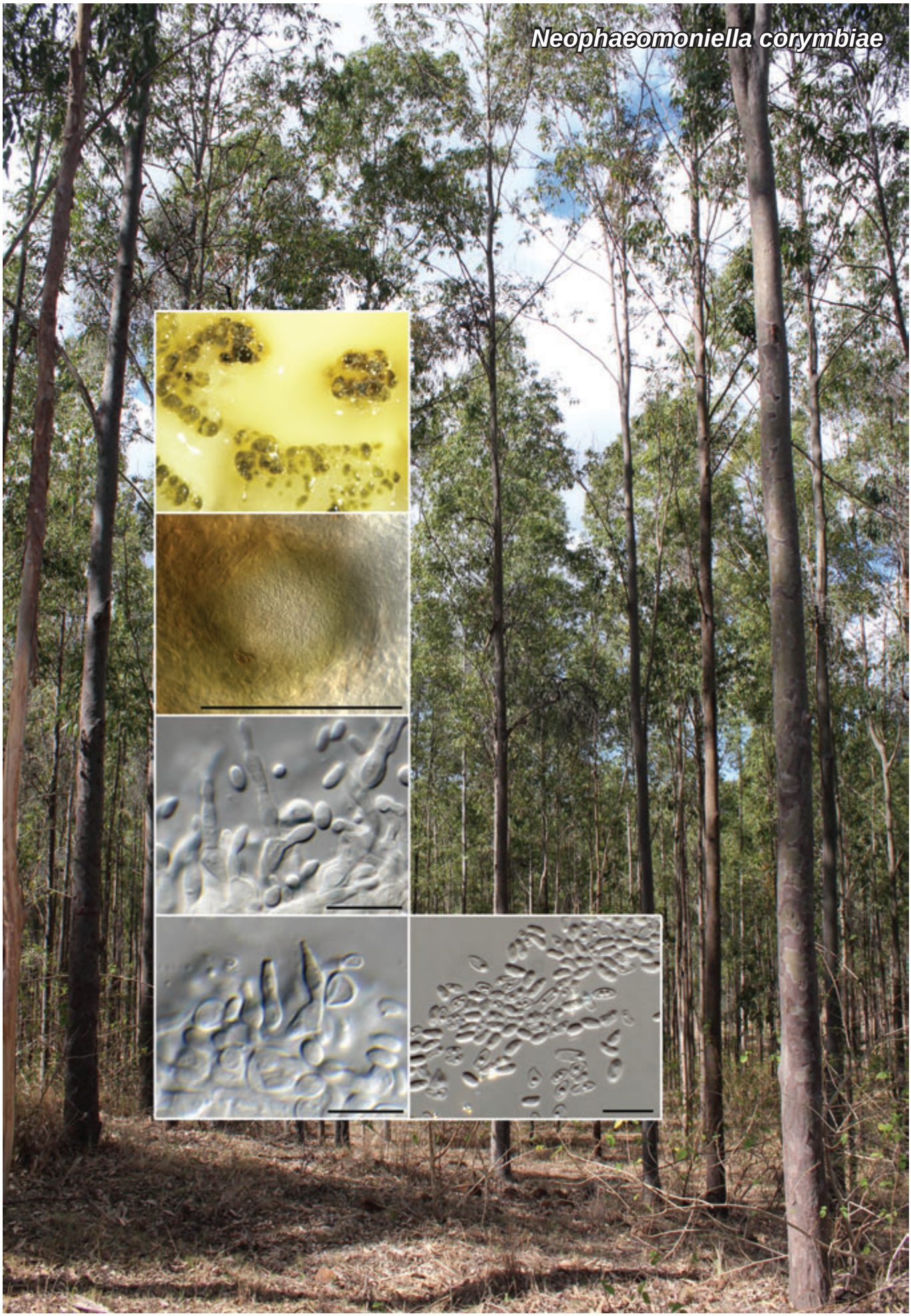
Neophaeomoniella corymbiae

Fungal Planet 819 – 14 December 2018

Neophaeomoniella corymbiae Crous, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was isolated.

Classification — *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes.*

Coelomycetous morph: *Conidiomata* pycnidial, olivaceous brown, globose, 100–200 µm diam with central ostiole. *Conidiophores* lining inner cavity, hyaline, smooth, branched, 0–1-septate, subcylindrical, 5–10 × 1.5–2 µm. *Conidiogenous cells* similar to those on hyphae. Hyphomycetous morph: *Mycelium* consisting of hyaline, smooth, 2–3 µm diam hyphae, branched, septate, encased in mucoid sheath. *Conidiophores* solitary, erect, subcylindrical, 1–2-septate, branched or not, 5–15 × 2–2.5 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to cymbiform, 5–7 × 2–2.5 µm, phialidic. *Conidia* aseptate, hyaline, smooth, subcylindrical to ellipsoid, apex obtuse, tapering at basal region to a truncate hilum, 0.5 µm diam, (3–)3.5–4(–5) × 1.5–2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, slimy, lacking aerial mycelium, surface folded, with smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

Typus. Australia, New South Wales, Dyraaba, Dyraaba plantation, on leaves of *Corymbia citriodora* (*Myrtaceae*), 14 Mar. 2015, *A.J. Carnegie*, HPC 2027 (holotype CBS H-23784, culture ex-type CPC 33273 = CBS 145092, ITS and LSU sequences GenBank MK047457.1 and MK047507.1, MycoBank MB828213).

Notes — The *Phaeomoniella* generic complex is commonly associated with brown wood streaking (Crous & Gams 2000, Halleen et al. 2007). Taxa in this complex have a hyphomycetous and yeast morph, with a coelomycetous synasexual morph. *Neophaeomoniella* (based on *N. eucalypti*) is a genus closely related to *Phaeomoniella* (Crous et al. 2015b), which has three species, isolated as endophytes from leaves and pine needles. *Neophaeomoniella corymbiae* was isolated from thyrothecial ascomata on leaves, although the sexual link is unconfirmed.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neophaeomoniella eucalypti* (GenBank NR_138001.1; Identities = 581/607 (96 %), 9 gaps (1 %)), *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044435.1; Identities = 550/579 (95 %), 10 gaps (1 %)) and *Neophaeomoniella zymoides* (GenBank KR909194.1; Identities = 568/601 (95 %), 9 gaps (1 %)). Closest hits using the **LSU** sequence are *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044454.1; Identities = 838/851 (98 %), no gaps), *Neophaeomoniella eucalypti* (GenBank NG_058174.1; Identities = 804/818 (98 %), 1 gap (0 %)) and *Neophaeomoniella zymoides* (GenBank MH874535.1; Identities = 832/851 (98 %), 3 gaps (0 %)).

Colour illustrations. *Corymbia citriodora*, Dyraaba plantation, Australia; colony sporulating on oatmeal agar, conidioma, conidiogenous cells and conidia. Scale bars: conidioma = 200 µm, all others = 10 µm.

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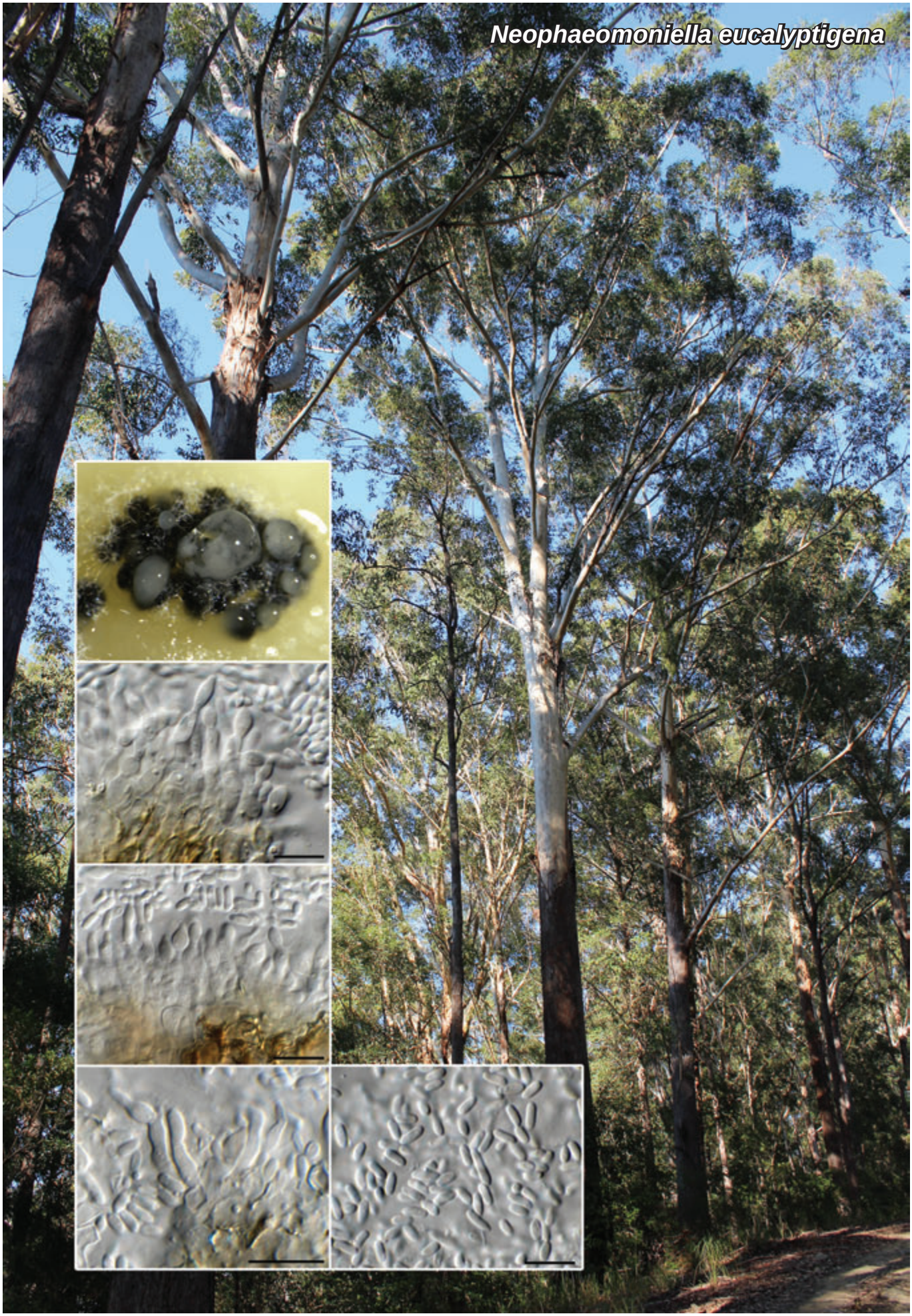
Neophaeomoniella eucalyptigena

Fungal Planet 820 – 14 December 2018

Neophaeomoniella eucalyptigena Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Classification — *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes.*

Conidiomata pycnidial, globose, brown, erumpent, 150–300 µm diam, exuding a creamy conidial mass. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 0–1-septate, branched or not, 5–10 × 2–2.5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to ampulliform, hyaline, smooth, phialidic, 4–6 × 2–2.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical, apex obtuse, tapering in lower region to truncate hilum, 0.5 µm diam, (3.5–)4–4.5(–5) × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, lacking aerial mycelium, surface folded, with smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse pale luteous. On PDA surface and reverse grey olivaceous in centre, cream in outer region. On OA surface cream to dirty white.

Typus. Australia, New South Wales, Coffs Harbour, Pine Creek State Forest, on leaf litter of *Eucalyptus pilularis* (*Myrtaceae*), Jan. 2015, *A.J. Carnegie*, HPC 2036 (holotype CBS H-23785, culture ex-type CPC 33358 = CBS 145093, ITS, LSU, *tef1* and *tub2* sequences GenBank MK047458.1, MK047508.1, MK047569.1 and MK047584.1, MycoBank MB828214).

Notes — *Neophaeomoniella eucalyptigena* is closely related to *N. corymbiae*, with both species being isolated from eucalypt leaves. Morphologically, they are very similar, and best distinguished based on their DNA data (579/607 (95 %) similar, including 10 gaps).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044435.1; Identities = 554/580 (96 %), 10 gaps (1 %)), *Neophaeomoniella eucalypti* (GenBank NR_138001.1; Identities = 577/607 (95 %), 9 gaps (1 %)) and *Neophaeomoniella zymoides* (GenBank KR909194.1; Identities = 574/604 (95 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044454.1; Identities = 852/863 (99 %), 1 gap (0 %)), *Neophaeomoniella eucalypti* (GenBank NG_058174.1; Identities = 807/818 (99 %), no gaps) and *Neophaeomoniella zymoides* (GenBank MH874535.1; Identities = 847/863 (98 %), 4 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phaeomoniella chlamydospora* (GenBank KP213113.1; Identities = 197/209 (94 %), no gaps) and *Pseudophaeomoniella oleae* (GenBank KP635968.1; Identities = 191/205 (93 %), no gaps). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. *Eucalyptus pilularis*, Pine Creek State Forest, Australia; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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Absidia terrestris

Fungal Planet 821 – 14 December 2018

Absidia terrestris Rosas de Paz, Dania García, Guarro, Cano & Stchigel, *sp. nov.*

Etymology. Referring to the substrate from which the fungus was recovered (soil).

Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycotina.*

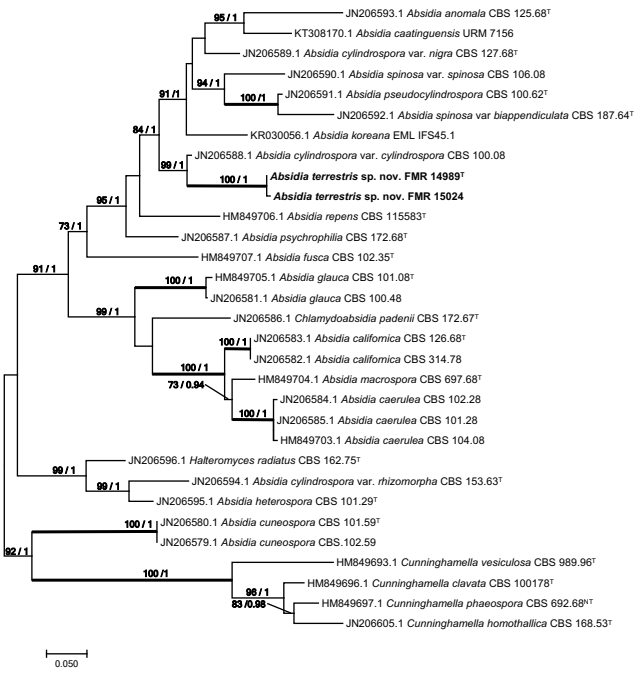
Hyphae hyaline to brownish, coenocytic, smooth- and thick-walled, 5–12.5 mm wide, with a septum at the branching site, usually filled with orange oil droplets and presenting more or less abundant solitary or catenulate ovoid swellings, 7.5–12.5 mm wide. *Stolons* hyaline to brownish, 5–14 mm wide. *Rhizoids* well developed, hyaline, originating along the stolon but never in the same place where sporangiophores arise. *Sporangiophores* hyaline to brownish, erect to slightly curved, smooth- and thick-walled, 25–215 × 2.5–5 mm, with a single septum below the sporangium and occasionally with an extra septum at the base when sporangiophores are short, arising along and terminally on the stolons and never grouped in whorls, swellings occasionally seen. *Sporangia* hyaline to brownish due to the mass of sporangiospores, pyriform, multispored, smooth-walled, apophysate, 17.5–27.5 × 17.5–22.5 mm. *Apophysis* funnel-shaped, smooth-walled, 12.5–17.5 × 7.5–12.5 mm. *Columellae* globose, smooth-walled, showing a short collarette, sometimes with a wall projection, 5–7.5 mm diam. *Sporangiospores* hyaline when solitary, brownish in mass when mature, smooth-walled, cylindrical, 4–5 × 2–4 mm. *Chlamydospores* absent. *Zygospores* not observed.

Culture characteristics — Colonies on MEA initially white, soon becoming greyish brown (M.6E3; Kornerup & Wanscher 1978), covering the diameter of the Petri dish (90 mm) in 7 d at 25 °C, reaching 10 mm height in some points; initially white, then becoming brownish grey (M.8F3). Minimum and maximum temperature of growth 15 and 27 °C, respectively.

Typus. Mexico, Mexico DF, Delegación Gustavo A. Madero, 'Corpus Christi' Public Park (19.467385–99.120635), from soil sample, 26 Aug. 2015, *E. Rosas de Paz* (holotype CBS H-23789, ex-type living culture FMR 14989, ITS and LSU sequences GenBank LT795003 and LT795005, MycoBank MB828081).

Additional material examined. Mexico, Mexico DF, Delegación Gustavo A. Madero, 'Los Cocodrilos' Public Park (19.475391–99.116705), from soil sample, 26 Aug. 2015, *E. Rosas de Paz*, living culture FMR 15024, ITS and LSU sequences GenBank LT795004 and LT795006).

Notes — This fungus was isolated from a soil sample collected in Mexico DF. Morphologically, *Absidia terrestris* resembles the species of *Absidia* s.str. with cylindrical sporangiospores (Hoffmann et al. 2007), i.e., *Absidia anomala*, *A. cylindrospora* var. *cylindrospora*, *A. pseudocylindrospora*, *A. psychrophilia*, *A. repens* and *A. spinosa.* Based on a megablast search of NCBIs GenBank nucleotide database using the ITS sequence of the isolate FMR 14989 (the ex-type strain), the closest hits are *A. cylindrospora* (GenBank AY944889.1; Identities 505/579 (87 %), 21 gaps (3 %)) and *A. spinosa* (GenBank AY944887.1; Identities 379/463 (82 %), 34 gaps 7 %)). The closest hits using the LSU sequence was *A. cylindrospora* var. *cylindrospora* (GenBank JN206588.1; Identities 620/657 (94 %), 5 gaps (0 %)). In a similar search using the CBS database (Crous et al. 2004), the closest hits using the LSU sequence of the isolate FMR 14989 were *A. spinosa* var. *spinosa* (CBS 106.08, Identities 308/406 (75.68 %), 9 gaps (2.2 %)), and *A. repens* (FSU 939, Identities 543/575 (94.43 %), 1 gap (0 %)). While using the ITS sequence the closest hits were *A. cylindrospora* var. *cylindrospora* (CBS 100.08, Identities 470/548 (86 %), 18 gaps (3 %)), and *A. pseudocylindrospora* (CBS 100.62, Identities 236/262 (90 %), 10 gaps (3 %)). Our phylogenetic tree, built using the LSU sequences, corroborated that our fungus represents a new species of the genus *Absidia*, *A. cylindrospora* var. *cylindrospora* being phylogenetically the most closely related species. *Absidia terrestris* differs from *A. cylindrospora* var. *cylindrospora* in its lower growth rate on MEA at 25 °C and in the absence of growth at 30 °C (*A. cylindrospora* var. *cylindrospora* grows up to 34 °C), the sporangiophores not arranged in whorls, the absence of chlamydospores and the presence of both apical and basal septa in the shorter sporangiophores.



Maximum likelihood (ML) tree obtained from the LSU sequence dataset of our isolates and sequences retrieved from GenBank. Fully supported branches (100 % ML bootstrap / 1.0 Bayesian posterior probability) are thickened. The novel species is indicated in **bold** face. The alignment was performed by using MEGA v. 6.06 (Tamura et al. 2013), and the tree was built by using MEGA v. 6.06 and MrBayes v. 3.2.4 (Huelsenbeck & Ronquist 2001). Ex-type strains of the different species are indicated with ^{T} or ^{NT}.

Colour illustrations. 'Corpus Christi' Public Park; colony on PDA, sporangiophore, columellae, sporangiospores. Scale bars = 15 µm, with the exception of the sporangiospores (= 5 µm).

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Amanita paludosa

Fungal Planet 822 – 14 December 2018

Amanita paludosa Bulyonk., Filippova & O.V. Morozova, *sp. nov.*

Etymology. The epithet *paludosa* (boggy) refers to the preferred habitat of the species.

Classification — *Amanitaceae*, *Agaricales*, *Agaricomycetes*.

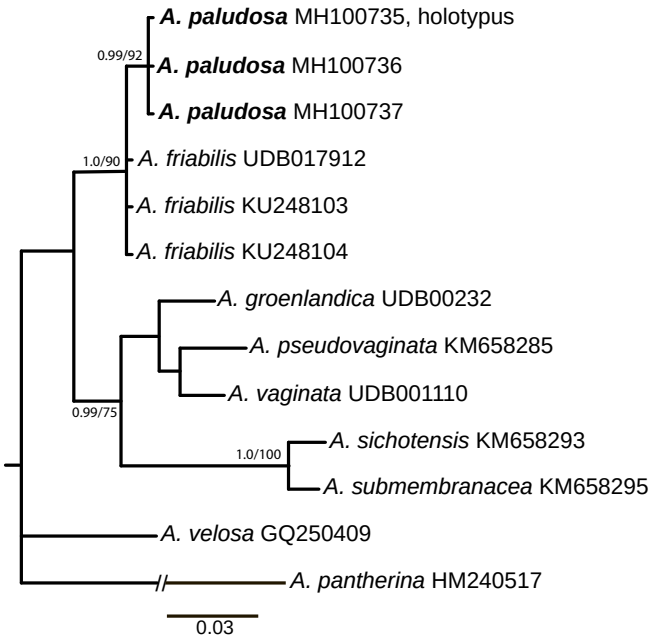
Cap 40–65 mm diam, planoconvex, obtusely umbonate, light brownish grey; surface glabrous, almost dry, ingrown-fibrillose under lens; margin very distinctly sulcate up to 5 mm with paler context showing between ribs. *Lamellae* subcrowded, off-white with light yellow-brown fimbriate edge concolorous with stipe apex, ventricose up to ± 7 mm, free. Universal veil fragments absent or present as a few small scattered greyish patches and warts. *Stipe* 70–90 × 10–17 mm, tapering upwards, with a broad rounded base but not bulbous; context white, firm, fistulose; surface light grey-brown and pruinose near apex, with paler zebroid fibrils below, in the lower third bearing fragments of volval material. *Volva* friable, up to 2 mm thick, brownish grey, appearing as wart-like floccules appressed to the stipe surface or partially or completely remaining bound to the substrate. *Pileipellis*: *suprapellis* an ixocutis of thin, filamentous hyaline hyphae in a gelatinous matrix; *subpellis* hyphae with yellow-grey intracellular pigment, some slightly constricted at septa, some forked, (2.9–)3.2–7.2(–8) µm (av. 5.4 µm) thick; vascular hyphae not plentiful, irregular, aseptate, present in all layers, 2–12 µm thick. *Lamella trama* bilateral. *Mediostratum* of well-inflated elements, filamentous hyphae scarce. *Lateral stratum* of inflated intercalary elements, appearing pseudoparenchymatous near lamellar base, closer to margin becoming mostly broadly ellipsoid and broadly fusiform, some branched and irregular-shaped, solitary and in chains of 2 or 3. *Subhymenium* near lamellar base virtually pseudoparenchymatous, of thin-walled, well-inflated elements, transitioning into the similarly well-inflated mediostratum; closer to the edge more structured, appearing as 2 or 3 layers of inflated, subglobose, angular or irregular ('jigsaw-puzzle'-like) elements. *Vascular hyphae* in lamella trama overall very rare, but common in the subhymenial layer of the lamella margin, where they sometimes form tangled masses of branching filamentous hyphae 2.5–3.2(–3.5) µm wide. *Inflated elements on the lamella margin* sphaeropedunculate, some utriform to broadly clavate, some slightly thick-walled, with pale greyish yellow intracellular pigment, 21.2–54.3 × 14.1–32.5 µm (av. L = 31.6, W = 22.0). *Universal veil* differentiated; outer layer dominated by sphaerocysts, some slightly collapsed, often in chains of 3 or 4, and often with pale yellowish grey intracellular pigment, linked by very thin, thin-walled, often collapsed, branching and forked filamentous hyphae; filamentous hyphae more abundant in the inner layer.

Colour illustrations. Top: treed transitional fen in Kondinskiye Ozera nature park in Yugra; bottom: bogged forest hollow in deciduous forest near Akademgorodok; inset: fruitbodies *ex situ* and *in situ*; detail of stipe base with veil and lamella margins; spores, veil with inflated elements; (all from holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores, veil).

Typus. Russia, Novosibirsk district, vicinity of Novosibirsk Akademgorodok, bogged hollow in mixed deciduous forest (*Betula pendula*, *Populus tremula*, *Salix* spp.), N54°50'55.38" E83°07'52.90", 9 Sept. 2011, *T. Bulyonkova* (holotype LE211974, ITS and LSU sequences GenBank MH100735 and MH100732, MycoBank MB825171).

Additional materials examined. Russia, KhMAO-Yugra, Kondinskiy district, Kondinskiye Ozera nature park, treed fen (*Betula* spp.), 1 Aug. 2008, *T. Bulyonkova*, LE311975; same location, 14 Aug. 2008, *T. Bulyonkova*, LE311976.

Notes — *Amanita paludosa* is a rare ringless *Amanita* so far known only from three collections along the Ob river basin, spanning across several hundred kilometres. The closest and most similar species is the European *A. friabilis*, mycorrhizal with *Alnus* in wetland habitats (Tulloss 2018). *Amanita paludosa* differs from *A. friabilis* by sparser and less fragmented velar remnants on pileus surface and stipe base due to its more differentiated veil structure with more abundant filamentous elements; markedly rounder, subglobose spores; mycorrhizal association with *Betula*; and a known distribution limited to West Siberia. Despite the proximity of the two taxa on molecular level, the significant differences in morphology, ecology, and distribution validate separating *A. paludosa* as a new species.



Phylogenetic tree derived from Bayesian analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed under GTR model, for 5 M generations, using MrBayes v. 3.2.1 (Ronquist et al. 2012). The ML analysis was run in the RAxML server (Stamatakis et al. 2008). Posterior probability (PP > 0.95) values from the Bayesian analysis followed by bootstrap support values from the Maximum Likelihood (BS > 50 %) analysis are added to the left of a node (PP/BS).

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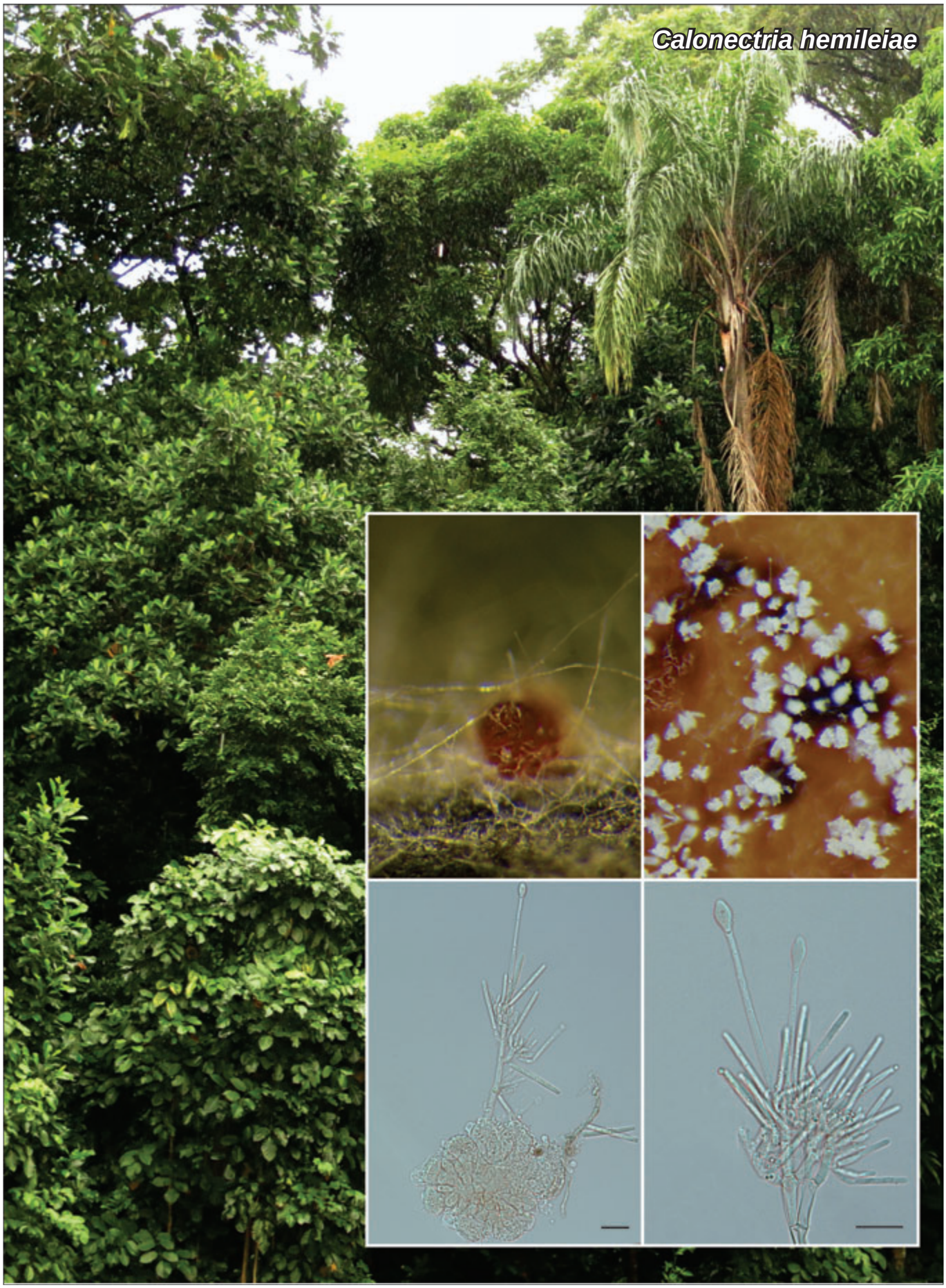

Calonectria hemileiae

Fungal Planet 823 – 14 December 2018

Calonectria hemileiae S.S. Salcedo, A.A. Colmán, H.C. Evans & R.W. Barreto, *sp. nov.*

Etymology. Named after its host, *Hemileia vastatrix*, the coffee leaf rust fungus.

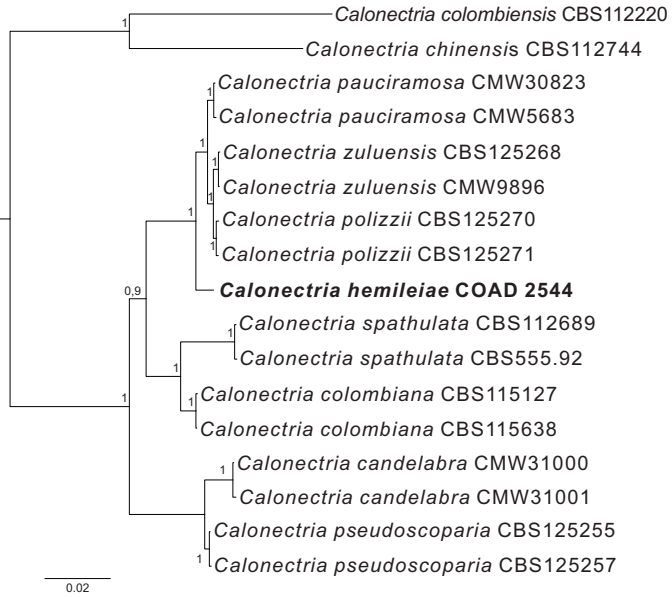
Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiophores erect, stipe bearing a penicillate arrangement of fertile branches followed by an extension with a terminal vesicle, smooth, hyaline. *Stipe* cylindrical, 120–220 × 3–8 µm; stipe extension cylindrical, straight to flexuous, 109–209 µm long, 2–4 µm wide at the apical septum, terminating in an obpyriform to fusoid vesicle, 5–10 µm diam. *Conidiogenous apparatus* penicillate, 45–75 µm long × 45–100 µm wide; primary branches, 8–27 × 3–6 µm, 0–1-septate; secondary branches, 8–18 × 3–7 µm, aseptate; tertiary branches, 6–14 × 3–5 µm, aseptate. *Conidiogenous cells* phialidic formed in groups of 2–6 at apex of terminal branches, elongate-doliiform to reniform, 5–13 × 2–4 µm, aseptate, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, straight, (35–)40–45(–48) × 3–5 µm (av. = 42 × 4 µm), rounded at both ends, 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Sexual morph* absent – only sterile perithecial-like structures formed in culture. *Mega-* and *microconidia* not seen. *Chlamydospores* catenulate, thick-walled, hyaline.

Culture characteristics — Fast growing (42–60 mm diam on malt extract agar (MEA), synthetic nutrient poor agar (SNA) and oatmeal agar (OA), after 7 d); low convex, margins entire, aerial mycelium cottony, white, bay or salmon, blood or bay reverse; sporulation sparse on MEA and OA and abundant in SNA; infertile perithecia and chlamydospores arranged in chains, produced throughout the medium and aggregating to form microsclerotia in SNA.

Typus. Brazil, state of Rio de Janeiro, Rio de Janeiro, on pustules of *Hemileia vastatrix* formed on leaves of *Coffea arabica*, 1 Sept. 2015, *R.W. Barreto* (holotype VIC 47145, ex-type culture COAD 2544, *tef1* sequences GenBank MK006026, *tub2* sequences GenBank MK037391, *his3* sequences GenBank MK006027 and *cal* sequences GenBank MK037392, MycoBank MB828262).

Notes — *Calonectria hemileiae* is a new member of the *C. candelabra* species complex (Alfenas et al. 2015, Lombard et al. 2015a, Lopes et al. 2018) based both on morphological characteristics and phylogenetic inference. The morphology of *C. hemileiae* is similar to that of *C. zuluensis* and *C. polizzii*. Nevertheless, it is clearly distinct from those taxa both in terms of ecological niche (the sole species of *Calonectria* recorded as a mycoparasite) and phylogenetically. Species of the *C. candelabra* complex are found worldwide, occurring on a range of plant hosts. Morphologically, they are characterised by having ellipsoidal to obpyriform vesicles, and 1-septate macroconidia (Schoch et al. 1999, Crous 2002, Lombard et al. 2010).



Consensus tree obtained by Bayesian Inference using the combined sequences of β-tubulin, translation elongation factor 1α, histone H3, and calmodulin gene regions of *Calonectria* spp. The tree was rooted to *C. chinensis* (CBS 112744) and *C. colombiensis* (CBS 112220). Bayesian posterior probabilities are given at the nodes and the accession numbers are presented together with the species names. Ex-type strain is indicated in **bold**.

Colour illustrations. Secondary Atlantic rainforest overgrowing old coffee plantation in Rio de Janeiro (Brazil); *Calonectria hemileiae* (ex-type COAD 2544); infertile perithecium, sporulating conidiophores giving rise to 1-septate macroconidia, *Hemileia vastatrix* urediniospore fascicle colonised by *Calonectria hemileiae*. Conidiogenous apparatus with variation in vesicle shape. Scale bars = 20 µm.

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Calvatia caatinguensis

Fungal Planet 824 – 14 December 2018

Calvatia caatinguensis R.L. Oliveira, R.J. Ferreira, B.D.B. Silva, M.P. Martín & Baseia, *sp. nov.*

Etymology. Referring to the biome in which it was collected.

Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

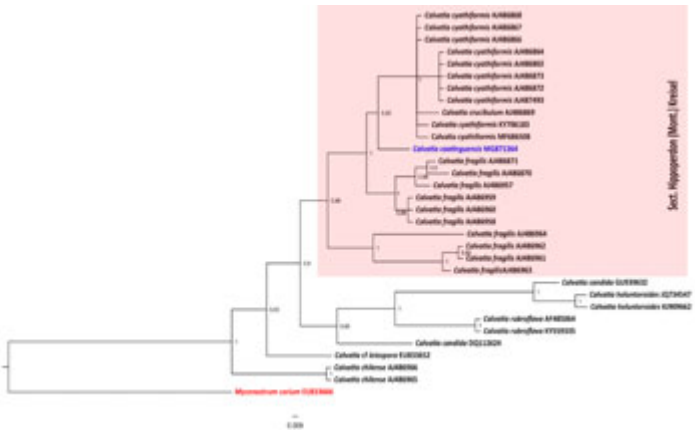
Basidiomata growing solitary, 35–40 mm wide × 45–58 mm high, pyriform to turbinate. *Exoperidium* slightly tomentose, evanescent, greyish brown (7E3, Kornerup & Wanscher 1978), at the base with sand encrusted at maturity. *Mesoperidium* membranaceous, smooth, greyish yellow to brown (4B4 to 5F5) at maturity. *Endoperidium* papyraceous externally, persistent in the basal portion, olive brown to brown (4E3 to 5E4). *Gleba* initially compact and white to yellowish white (4A1 to 4A2), becoming lanose and powdery, brownish grey to dark brown (5D2 to 9F4) at maturity. *Subgleba* well-developed, occupying two thirds of the basidioma, when mature pale yellow at base to dark brown going up (4A3 to 6F8), and presenting a different colour band, yellowish white (4A2) at the apex of subgleba. *Rhizomorphs* densely encrusted with sand, 2.5–6.2 µm diam, regular walls ≤ 1.3 µm thick, curved, branched, septate, hyaline in 5 % KOH, and dextrinoid. *Exoperidium* composed for hyphae, 2.7–4.5 µm diam, with regular walls ≤ 0.7 µm thick, straight, rarely branched and septate, hyaline in 5 % KOH and not dextrinoid. *Endoperidium* with hyphae 2.8–5.1 µm diam, with regular walls ≤ 1.16 µm thick, straight, branched, frequently septate, pale brown in 5 % KOH, and dextrinoid; presence of mycosclereids globose, subglobose, pyriform, triangular, ovoid, ellipsoid or rectangular shape, present in the apical portion, 14.4–29.5 × 7.6–17.8 µm, with regular walls ≤ 1.35 thick, and straight. *Subgleba* with hyphae measuring 2.3–4.2 µm diam, with regular walls ≤ 1.2 µm thick, curved, branched, septate, hyaline in 5 % KOH, and dextrinoid. *Paracapillitium* absent. *Capillitium Calvatia*-type, hyphae 2.7–4.5 µm diam with regular walls ≤ 0.88 µm thick, straight, frequently branched, septate, with small and numerous circular pits, hyaline in 5 % KOH, dextrinoid. *Basidiospores* subglobose, equinulated, 5.4–7.4 × 5.1–6.7 µm [χ = 5.9 ± 0.5 × 5.6 ± 0.4; Q_m = 1.06; n = 20], pedicels present in some spores, ≤ 1.09 µm, hyaline in 5 % KOH, dextrinoid and acyanophilic.

Habit & Habitat — Growing solitary or two basidiomata on decaying leaves.

Typus. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, near trail, soil, Feb. 2017, *R.L. Oliveira* (holotype UFRN fungos 2945, ITS and LSU sequences GenBank MG871364 and MH988750, MycoBank MB824127).

Notes — *Calvatia caatinguensis* is a typical species in section *Hippoperdon*. Based on morphological and molecular characters, it is closely related to some other *Calvatia* species, such as *C. crucibulum*, *C. cyathiformis*, *C. fragilis* and *C. lilacina*.

Calvatia fragilis has a lycoperdon-type capillitium with numerous small circular pits; however, *C. fragilis* does not have a subgleba or it is reduced, and basidiospores are smaller and finely equinulated (Morgan 1890, Silveira 1943). *Calvatia crucibulum*, a species reported only by Kreisel (1992, 1994), has similar morphological characteristics, such as a capillitium with small and numerous pits, woolly gleba, and fine exoperidium. However, in those publications the author does not describe some macroscopic (subgleba) and microscopic structures (basidiospores), which makes a comparison difficult. In the present study these two species are well separated by their ITS nrDNA barcode sequences. *Calvatia lilacina* is another morphologically similar species to *C. caatinguensis*, mainly based on the distinct colour band at the apex of the subgleba; however, *C. lilacina* has smaller basidiospores (3–5 µm), which are verrucose to spinulose (Bottomley 1948). In recent decades, *C. fragilis* and *C. lilacina* have been considered by some researchers as synonyms of *C. cyathiformis* (Bottomley 1948, Zeller & Smith 1964, Liu 1984, Moyersoen & Demoulin 1996, Poumarat 2003, Wartchow & Silva 2007), while others have considered *C. lilacina* as a synonym of *C. fragilis* (Kreisel 1992, 1994). *Calvatia cyathiformis* is recognised by the violaceous gleba, pulverulent, verrucose to echinate basidiospores, subgleba cellular and well developed, capillitium long, branched and with numerous circular pits (Dissing & Lange 1962, Zeller & Smith 1964). This species has been reported in several parts of the world (Morgan 1890, Dissing & Lange 1962, Zeller & Smith 1964, Liu 1984, Moyersoen & Demoulin 1996, Poumarat 2003), including Brazil (Silveira 1943, Viégas 1945, Wartchow & Silva 2007). *Calvatia cyathiformis* is characterised by a marked morphological variation in basidiospores and capillitium. However, *C. caatinguensis* has a distinct colour band at the apex of the subgleba, in addition to a marked encrustation at the basal exoperidium when mature, not observed in *C. cyathiformis*. Morphological and molecular data (ITS nrDNA) provide strong support for *C. caatinguensis* as a distinct species of *Calvatia*.



Colour illustrations. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, where the specimens were collected; immature basidiome *in situ* (UFRN-Fungi 2946); longitudinal section through mature basidiome (UFRN-Fungi 2945); mature basidiome *in situ* (UFRN-Fungi 2945); capillitium under SEM (UFRN-Fungi 2266); basidiospores under SEM (UFRN-Fungi 2266). Scale bars = 10 mm (basidiomata), 1 µm (basidiospores and capillitium).

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Carolinigaster bonitoi

Fungal Planet 825 – 14 December 2018

Carolinigaster M.E. Sm. & S. Cruz, *gen. nov.*

Etymology. The genus name *Carolinigaster* refers to North Carolina, the region where this truffle was collected, and 'gaster' (Greek for 'stomach') in reference to the fact that the spores of this truffle species are enclosed inside of the fruiting body.

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes.*

Distinguished from other *Boletaceae* by a combination of the following characters: *Basidiomata* hypogeous to partially emergent, sequestrate, globose to subglobose. *Peridium* not changing colour when handled. *Gleba* loculate. Lacking a stipe or columella. *Basidiospores* statismosporic, globose to subglobose, ornamented with short irregular warts at maturity, pink in water and inamyloid but strongly dextrinoid, bleaching to almost hyaline in KOH. *Clamp connections* and *hymenial cystidia* absent.

Type species. *Carolinigaster bonitoi* M.E. Sm. & S. Cruz.
MycoBank MB827451.

Carolinigaster bonitoi M.E. Sm. & S. Cruz, *sp. nov.*

Etymology. The epithet *bonitoi* is given in reference to mycologist Gregory Bonito – a truffle expert, North Carolina native, and co-collector of the type specimen.

Basidiomata hypogeous, globose to subglobose, 0.5–2 cm diam, attached to the substrate by fine white rhizomorphs. *Peridium* bright white to pinkish white, completely enclosing the gleba when young but thinning and wearing away with age, not changing colour when handled or bruised. *Gleba* loculate, locules up to 0.5 mm diam but mostly 0.25 mm or smaller, light pink when young but becoming pinkish brown to light brown in mature specimens, rubbery when fresh. Lacking a columella or sterile base. *Odour* indistinct, *taste* not recorded. *Peridium* 50–210 µm thick, hyaline, comprised of loosely interwoven gelatinised hyphae mostly 5 µm diam, notably softer in 3 % KOH than in water or Melzer's, with occasional incorporated rhizomorphs up to 10 µm diam and slightly dextrinoid. *Basidia* 40–55 × 10–15 µm but narrowing to 5 µm at the base, four-spored, clavate to subcapitate and scattered. Sterigmata mostly 5–6.5 µm long and 0.5–1 µm diam. *Trama* tissues appearing gelatinised, especially when mounted in KOH. *Basidioles* numerous, hyaline, clavate or occasionally subcapitate, 30–45 × 8–13 µm wide, narrowing to 3.5–4.5 µm at the base. *Clamp connections* not observed. *Cystidia* not observed. *Basidiospores* statismosporic, 8.8–11 × 5.9–8.4 µm (av. 9.7 × 7.3 µm), Q = 1.2–1.8 (mean Q = 1.35), globose to subglobose, pink in water, inamyloid and strongly dextrinoid in Melzer's reagent, bleaching to almost hyaline in KOH, spore wall mostly 1 µm, ornamented with triangular to rounded warts that are 0.5–1.5 µm tall × 1–2 µm wide at the base, with a hyaline perispore that is always visible in young spores but is more difficult to see in mature spores, often with a visible hilar appendage that is approximately 0.5 µm diam and 1–2 µm long.

Habitat & Distribution — Fruiting in the soil beneath the leaf litter in mixed forests dominated primarily by *Quercus*, *Fagus* and *Pinus* on silty-clay soil. Known only from Durham County but likely present at appropriate sites across North Carolina's Piedmont region.

Typus. USA, North Carolina, Durham County, Durham, Duke University Campus, c. 150 m a.s.l., in mixed pine and hardwood forest, hypogeous in soil below the leaf litter, 21 Oct. 2009, *G. Bonito & J. Trappe* MES331 (holotype FLAS-F-62017, ITS, LSU and *tef1* sequences GenBank MH747178, MH747179 and MH753704, MycoBank MB827455).

Additional specimen examined. USA, North Carolina, Durham County, Durham, Eno River State Park, c. 200 m a.s.l., in mixed pine and hardwood forest, hypogeous in soil below the leaf litter, 16 Oct. 2009, *M.E. Smith*, MES330, FLAS-F-62018.

Colour illustrations. Mixed *Fagaceae*-dominated forest near in Durham, North Carolina where *Carolinigaster bonitoi* was collected; section of hyaline trama viewed in Melzer's reagent (scale bar = 25 µm), basidiospores showing strong dextrinoid responses when viewed in Melzer's reagent (scale bar = 10 µm), fresh basidiomata (scale bar = 1 cm). All photos are of the holotype MES331 (FLAS-F-62017).

Notes — *Carolinigaster bonitoi* is unique in having a hypogeous sequestrate fruiting habit, a bright white peridium that does not stain when handled or bruised, and a loculate gleba without a columella or sterile base that is light pink when young but becomes pinkish brown to brown at maturity. It has lightly ornamented spores covered by a perisporium. The spores are pinkish in water and strongly dextrinoid in Melzer's reagent but bleach almost completely hyaline in 3 % KOH.

Carolinigaster bonitoi is related to species of *Austroboletus*, *Fistulinella*, *Veloporphyrellus* and *Mucilopilus* in the *Austroboletoideae*. *Mucilopilus castaneiceps* forms a sister clade to *C. bonitoi* but without support. *Mucilopilus castaneiceps* is a Japanese epigeous bolete that is superficially quite different from *C. bonitoi* but it actually shares some important features. Both taxa have dextrinoid spores, both have hymenial surfaces that are light when young but become dark pink or pinkish brown at maturity, and both fruit in association with trees in the *Fagaceae* (Takahashi 1988). The only other known truffle in the *Austroboletoideae* is *Solioccasus polychromus* (Trappe et al. 2013, Wu et al. 2016). *Solioccasus polychromus* is a brightly coloured tropical associate of *Myrtaceae* and *Fabaceae* that has smooth ellipsoid spores and is known only from Australasia.

No other bolete truffle has all of the same morphological features as *C. bonitoi* but the most similar taxon is *Jimtrappea guyanensis* (Smith et al. 2015). However, *J. guyanensis* is phylogenetically distant and has large, amyloid hymenial cystidia and smooth fusoid spores that are not dextrinoid, and is restricted to *Dicymbe*-dominated forests in Guyana.

Carolinigaster bonitoi is thus far known only from two collections from mixed, *Fagaceae*-dominated forests in North Carolina, USA. It is interesting that this species has not been found previously, particularly since Coker & Couch (1928) extensively studied the gasteromycetes (including hypogeous sequestrate species) of North Carolina. Coker & Couch (1928) recognized 26 species of '*Hymenogasteraceae*' in their book but none of the species they studied are similar to *C. bonitoi*.

For supplementary information see MycoBank.

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Cercospora solani-betacei

Fungal Planet 826 – 14 December 2018

Cercospora solani-betacei B.W. Ferreira & R.W. Barreto, *sp. nov.*

Etymology. Referring to the host, *Solanum betaceum*, from which it was described.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

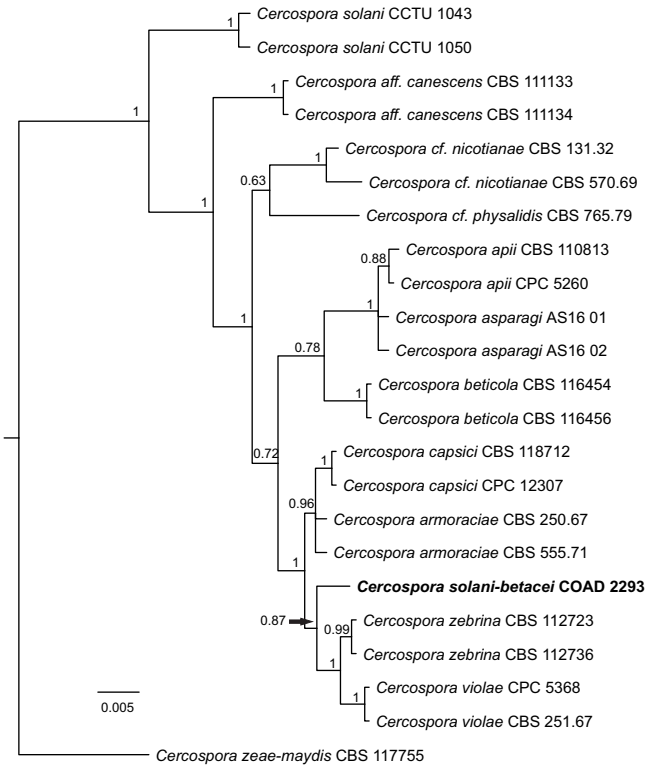
Lesion on living leaves, starting as small necrotic dots, becoming sub-circular, to irregular, 5–15 mm diam, brown, with dark brown margins, coalescing and leading to extensive blight. *Internal mycelium* indistinct. *Stromata* reduced to few angular cells, 12–25 × 35–55 µm. *Conidiophores* predominantly hypophyllous, rarely epiphyllous, in fascicles of 5–22 conidiophores, sub-cylindrical, geniculate, 100–172 × 4–5 µm, 3–7-septate, unbranched, pale olivaceous brown, smooth. *Conidiogenous cells* terminal, subcylindrical, sympodial, sub-hyaline, 15–65 × 3–5 µm. *Conidiogenous loci* conspicuous, 2–3 µm diam, strongly thickened, darkened. *Conidia* obclavate to subcylindrical, straight to slightly curved, 47–130 × 3–5 µm, apex rounded to subacute, base truncate, 3–12-septate, guttulate, hyaline, smooth.

Culture characteristics — Slow-growing (45 mm in PDA and 35 mm in PCA, after 15 d) at 25 °C. Colony sub-umbonate, edge entire, aerial mycelium dense and felty, white; in PDA radially sulcate. Reverse rosy buff with concentric haloes olivaceous. Sporulation absent.

Typus. Brazil, Minas Gerais, Antônio Carlos, Dr. Sá Fortes, on living leaves of *Solanum betaceum* (tree tomato), 10 June 2017, *B.W. Ferreira* (holotype VIC 44319, ex-type culture COAD 2293, ITS, LSU, *cmdA* and *actA* sequences GenBank MH223464, MH700245, MH428037 and MH445457, MycoBank MB826812).

Notes — A *Cercospora* sp. has been reported on *Cyphomandra betacea* (= *S. betaceum*) in Malawi (Peregrine & Siddiqi 1972) and Zimbabwe (Whiteside 1966). Other records of *Cercospora* spp. on members of *Solanum* spp. are: *Cercospora apii*, *C. canescens*, *C. cyperacearum*, *C. lanugiflori*, *C. physalidis*, *C. puyana*, *C. solanacea*, *C. solani*, *C. solanicola*, *C. solanigena* (Farr & Rossman 2018). The morphology of the *Cercospora* on tree tomato was similar to that of species belonging to the *C. apii* complex (Groenewald et al. 2013). A BLASTn search on GenBank indicated a considerable similarity of *C. solani-betacei* to other species belonging to *Cercospora*. A concatenated phylogenetic tree was constructed with ITS, *cmdA* and *actA* and, the combined result clearly supported *S. betaceum* as a distinct species.

Koch's postulates were performed and the pathogenicity of the fungus to *S. betaceum* was demonstrated.



Phylogenetic tree inferred from Bayesian analysis based on concatenated sequences (ITS, *cmdA* and *actA*). The analysis was performed with 10 million generations in MrBayes v. 3.1.1. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Cercospora zeae-maydis*. The new species is highlighted in **bold** face.

Colour illustrations. *Solanum betaceum* in subsistence orchard; leaf spots on *S. betaceum*, *Cercospora solani-betacei* conidiophore fascicle and conidia. Scale bars = 40 µm (conidiophores) and 10 µm (conidia).

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Acaulium pannemaniae

Fungal Planet 827 – 14 December 2018

Acaulium pannemaniae Sandoval-Denis, *sp. nov*.

Etymology. Named after Amina Panneman, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Microascaceae*, *Microascales*, *Sordariomycetes*.

Colonies on OA at 25 °C attaining 18–24 mm in 14 d, ochreous to buff coloured, flat, membranous with regular margins. On PDA at 25 °C attaining 13–15 mm in 14 d, white to light buff, flat, fluffy to dusty with membranous periphery and regular margins. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled. *Conidiophores* mononematous, penicillate branched; irregularly bi- to terverticillate, bearing groups of 2–4 conidiogenous cells, rarely reduced to single conidiogenous cells borne laterally on the aerial hyphae, hyaline to subhyaline, smooth-walled. *Conidiogenous cells* percurrent, lageniform to ampulliform, (11–)13.5–29(–44) × 3–4.5 µm, 21.4 ± 7.5 × 3.9 ± 0.3 µm long, broad at the widest part, tapering to a long cylindrical, annellated zone, 1.5–2.5 µm wide, up to 23 µm long, annellations inconspicuous. *Conidia* bullet-shaped or broadly clavate, (5.5–)6.5–10.5(–13) × (2.5–)3–4(–5), 8.6 ± 1.7 × 3.5 ± 0.4 µm, with a distinctive truncate base and rounded or slightly pointed apex, subhyaline to pale brown in mass, smooth- or finely roughened, thick-walled, arranged in long chains.

Typus. The Netherlands, Gelderland, Kapel-Avezaath, from soil under wooden chippings, 2017, *A. Panneman* (holotype CBS H-23741, culture ex-type CBS 145025 = JW79009; ITS, LSU, *tef1* and *tub* sequences GenBank LS999990, LS999991, LS999992 and LS999993, MycoBank MB827981).

Notes — The genus *Acaulium* was recently reinstated and segregated from *Scopulariopsis* (Sandoval-Denis et al. 2016). Four species are currently accepted (Woudenberg et al. 2017). *Acaulium pannemaniae* closely resembles *Acaulium album*. However, the new species differ by producing mononematous conidiophores only in contrast to the synnematous conidiophores of *A. album*. *Acaulium pannemamiae* also exhibits much larger conidiogenous cells, often with exceptionally long annellated necks which also contrast with all other known species of the genus.

Colour illustrations. Background, collection site; branched conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Gibellulopsis simonii

Fungal Planet 828 – 14 December 2018

Gibellulopsis simonii Giraldo López, *sp. nov.*

Etymology. *simonii*, refers to the name of the collector of the ex-type strain, Simon van Stuijvenberg. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

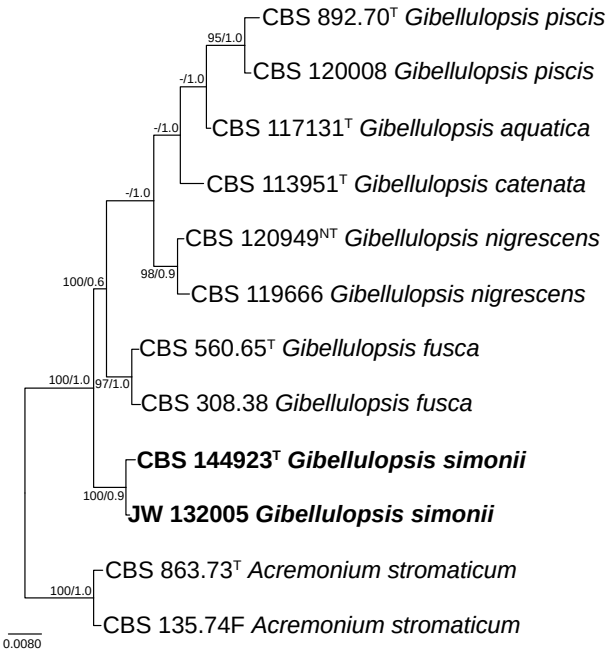
Classification — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes.*

Mycelium consisting of branched, septate, smooth, hyaline and thin-walled hyphae, up to 2 µm wide. *Conidiophores* simple or poorly branched, hyaline, smooth-walled, up to 83 µm long. *Phialides* lateral or terminal, subcylindrical to subulate, hyaline, smooth, 17–46 × 1.5–2 µm, with minute cylindrical collarette and periclinal thickening at the conidiogenous locus. *Conidia* cylindrical or ellipsoidal, sometimes with a slightly truncate base, 1-celled, hyaline, thin- and smooth-walled, 3.5–6 × 1.5–2 µm, arranged in slimy heads. *Chlamydospores* lateral or intercalary, single, with or without intermittent hyaline cells, subglobose or clavate, brown, smooth- and thick-walled, 4–7 × 3.5–5.5 µm.

Culture characteristics — Colonies on OA and PDA after 10 d at c. 25 °C, reaching 25–27 and 28–29 mm diam, respectively, flat, surface and reverse dark mouse grey to fuscous black, with a pale mouse grey mycelium forming concentric rings.

Typus. The Netherlands, Gelderland, Meteren, isolated from soil, 2017, coll. *S. van Stuijvenberg*, isol. *A. Giraldo* (holotype CBS H-23735, cultures ex-type CBS 144923 = JW132008, ITS and LSU sequences GenBank MK047467.1 and MK047517.1, MycoBank MB828025).

Notes — *Gibellulopsis* species are commonly soil-borne fungi, morphologically characterised by sparse branched conidiophores, ellipsoidal to cylindrical conidia and olive-brown chlamydospores (Domsch et al. 2007). Batista & Maia (1959) introduced the genus based on *G. piscis*, which was subsequently synonymised with *Verticillium nigrescens* (Zare et al. 2007). The genus was recently revised, and five species were accepted. *Gibellulopsis chrysanthemy* (Hirooka et al. 2014) was segregated from *Gibellulopsis* and accommodated elsewhere (Giraldo & Crous 2019). Morphologically, *G. simonii* resembles *G. nigrescens* in having lateral or intercalary subglobose chlamydospores. *Gibellulopsis simonii,* however, produces shorter and less branched conidiophores than those of *G. nigrescens* (up to 100 µm long), and is phylogenetically different from the ex-type strain of that species.



Bayesian inference tree based on ITS sequences from *Gibellulopsis* species. RAxML v. 8.2.10 bootstrap values above 70 % and Bayesian posterior probabilities are shown at the nodes. The tree was rooted to *Acremonium stromaticum*. The new species described here is shown in **bold** face. T Ex-type, NT Ex-neotype.

Colour illustrations. Garden where the soil sample was collected; conidiophores, conidia and chlamydospores. Scale bars: = 10 µm (conidiophores and conidia) and 5 µm (chlamydospores).

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Fusicolla septimanifiniscientiae

Fungal Planet 829 – 14 December 2018

Fusicolla septimanifiniscientiae L. Lombard & Hern.-Restr., *sp. nov*.

Etymology. From Latin *septimana*- meaning week, *fini*- meaning the end of, and *scientiae*- meaning science. Named after the 'Weekend of Science'.

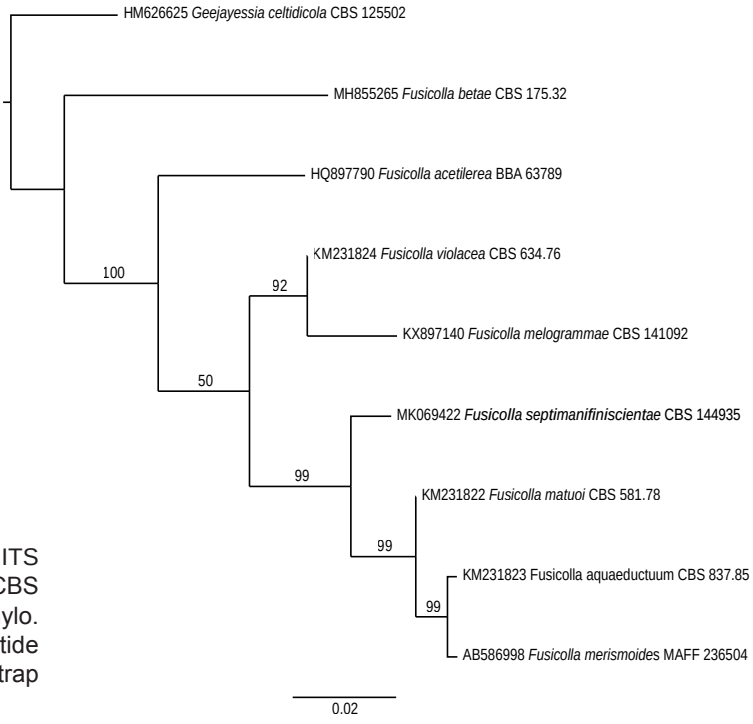
Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiophores initially as lateral phialides arising directly from somatic hyphae, simple or rarely branched, monochasial or verticillate, straight, hyaline, smooth-walled, aseptate or with basal septum, up to 32 µm long. *Conidiogenous cells* monophialidic or rarely polyphialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, cylindrical to subulate, 6–16 × 3–4 µm, thin- and smooth-walled, hyaline with inconspicuous collarettes and periclinal thickening. *Macroconidia* falcate, more or less straight, slightly narrowing towards the ends, apical cell often hooked with a more or less pointed tip, basal cell slightly pedicellate, (1–)3-septate, (19–)25–29(–34) × 3–4 µm (av. 27 × 3 µm), hyaline, thin- and smooth-walled. *Microconidia* absent. *Chlamydospores* single or in pairs, intercalary or terminal, globose to obovoid, thick-walled and verruculose. *Sexual morph* unknown.

Culture characteristics — Colonies on OA, MEA and PDA at 25 °C attaining 25–30 mm in 7 d. On OA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, buff to primrose, margin entire. On MEA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, rosy buff to buff, reverse buff, margin entire. On PDA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, pale luteous to buff, reverse pale luteous, margin entire.

Typus. The Netherlands, Utrecht Science Park, Westerdijk Fungal Biodiversity Institute, from soil in front of the bronze statue of Johanna Westerdijk, Mar. 2017, *M. Hernandez-Restrepo* (holotype CBS H-23749, culture ex-type CBS 144935); ITS, LSU, *tef1* and *tub2* sequences GenBank MK069422, MK069418, MK077808 and MK069408, MycoBank MB828215).

Notes — *Fusarium* s.lat. has recently been segregated into several fusarium-like genera, one of which is *Fusicolla* (Lombard et al. 2015b, Guarnaccia et al. 2018). *Fusicolla septimanifiniscientiae* can be distinguished from other species in the genus *Fusicolla* by the formation of polyphialidic conidiogenous cells on the somatic hyphae (Gräfenhan et al. 2011). Based on phylogenetic inference of the ITS sequences, *F. septimanifiniscientiae* is closely related to *F. aquaeductuum*, *F. matuoi* and *F. merismoides*. However, *F. septimanifiniscientiae* mostly produced 3-septate macroconidia ((19–)25–29(–34) × 3–4 µm (av. 27 × 3 µm)), rarely 1-septate, which are smaller than the 3-septate macroconidia of *F. aquaeductuum* (30–55 × 2.5–3.5 µm; Gerlach & Nirenberg 1982), *F. matuoi* ((25–)33–56 × (1.5–)2–3 µm; Hosoya & Tubaki 2004) and *F. merismoides* (26–48 × 3–4.3 µm; Gerlach & Nirenberg 1982).



Maximum likelihood phylogeny of *Fusicolla* inferred from ITS sequences. The tree is rooted to *Geejayessia celtidicola* (CBS 125502). Analysis preformed online in CIPRES (www.phylo.org) using RAxML BlackBox using the GTR+I+G nucleotide substitution model. Branch support assessed using bootstrap with replicates determined by the software.

Colour illustrations. Background, collection site (grounds of the Westerdijk Fungal Biodiversity Institute); conidiophores, mono- and polyphialidic conidiogenous cells, macroconidia and chlamydospores. Scale bars = 10 µm

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Lasionectria hilhorstii

Fungal Planet 830 – 14 December 2018

Lasionectria hilhorstii L. Lombard, *sp. nov*.

Etymology. Named for Tjidde Hilhorst, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Bionectriaceae*, *Hypocreales*, *Sordariomycetes*.

Colonies on OA at 25 °C attaining 12–20 mm in 7 d, aerial mycelium collapsed with abundant sporulation on the medium surface forming vinaceous green to vinaceous black droplets of conidial masses, margin undulate surrounded by a vinaceous to greyish rose halo, surface vinaceous black, reverse isabelline in the centre becoming vinaceous towards the margins. On MEA at 25 °C attaining 20–25 mm in 7 d, with moderate aerial mycelium, felty with string folds into the medium, margin undulate, surface olivaceous black in the centre due to abundant sporulation becoming brick to rosy vinaceous towards the margin, surrounded by a vinaceous halo, reverse vinaceous to rosy buff. *Sexual morph* not seen. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, becoming slightly verrucose with age, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae, simple or branched, straight, hyaline and smooth-walled becoming slightly verrucose and subhyaline with age, aseptate or with basal septum, up to 56 µm long. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monophialidic, aseptate, elongate-ampulliform to subcylindrical, 13–24 µm long, 1–3 µm wide at the base, thin- and smooth-walled to slightly verrucose, hyaline to subhyaline with inconspicuous collarettes and periclinal thickening. *Conidia* unicellular, ovoid to broadly ellipsoidal, 3–5 × 2–3 µm (av. 4 × 2 µm), subhyaline to olivaceous green, thick- and smooth-walled, forming slimy heads on the phialides. *Chlamydospores* not seen.

Typus. The Netherlands, Gelderland, Eibergen, from soil, Mar. 2017, *T. Hilhorst* (holotype CBS H-23747, culture ex-type CBS 144938 = JW85024; ITS, LSU, *act* and *tef1* sequences GenBank MK069421, MK0269417, MK069414 and MK069411, MycoBank MB828216).

Notes — *Lasionectria hilhorstii* is morphologically reminiscent of *Acremonium cereale* (Gams 1971), but can be distinguished by the lack of flared collarettes and basal swelling of the phialides. Additionally, megablast searches of NCBIs GenBank nucleotide database using LSU sequences indicated that the closest species were *L. oenanthicola* (GenBank KY607557.1; Identities = 839/839 (100 %), no gaps), *A. cereale* (GenBank MH877716.1; 839/840 (99 %), 1 gap) and *L. mantuana* (GenBank GQ505994.1; Identities = 838/839 (99 %), no gaps). The closest hits using ITS sequences were *L. oenanthicola* (GenBank KY607542.1; 864/898 (96 %), 14 gaps (1 %)), *A. persicinum* (GenBank KM030294.1; 782/851 (92 %), 25 gaps (2 %)) and *Ijuhya dentifera* (GenBank KY607540.1; 793/869 (91 %), 21 gaps (2 %)). The closest hits using *act* sequences were *Gliocladium* sp. (GenBank KY608883.1; 606/650 (93 %), 7 gaps (1 %)), *Clonostachys rosea* (GenBank KP274072.1; 605/652 (93 %), 7 gaps (1 %)) and *Alternaria hyacinthi* (GenBank JQ671603.1; 604/653 (92 %), 7 gaps (1 %)). The closest hits using *rpb2* sequences were *Septofusidium berolinense* (GenBank KM232417.1; 699/856 (82 %), 11 gaps (1 %)), *Heleococcum aurantiacum* (GenBank JX158463.1; 701/861 (81 %), 11 gaps (1 %)) and *Stromatonectria caraganae* (GenBank HQ112290.1; 688/857 (80 %), 10 gaps (1 %)). The closest hits using *tef1* sequences were *L. mantuana* (GenBank HM484844.1; 376/398 (94 %), 2 gaps (0 %)), *Neocosmospora* sp. (GenBank LT746219.1; 229/263 (87 %), 11 gaps (4 %)) and *Hydropisphaera* sp. (GenBank HM484845.1; 232/268 (87 %), 13 gaps (4 %)).

Colour illustrations. Background, collection site (backyard); conidiophores and conidia. Scale bars = 10 µm.

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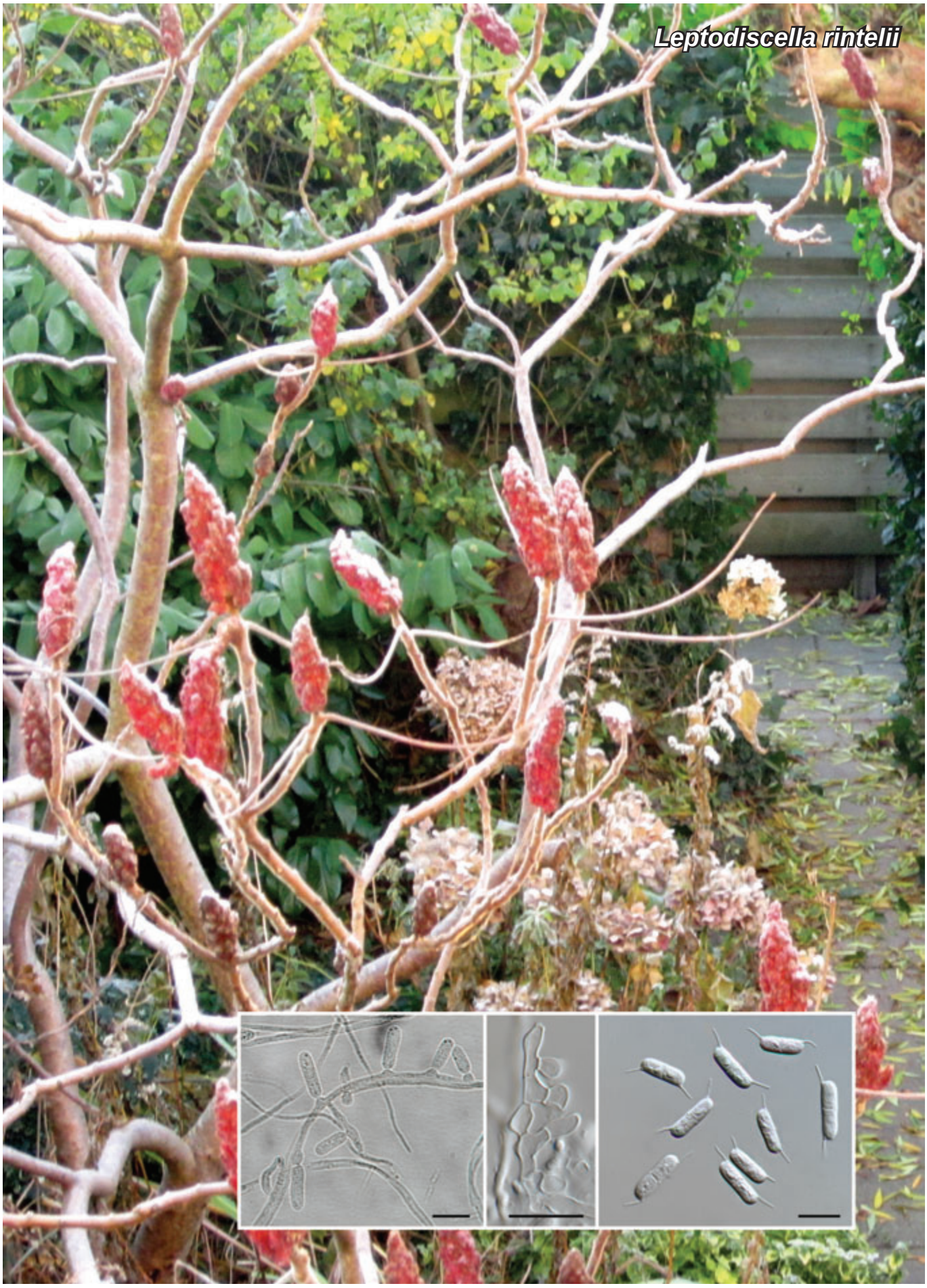
Leptodiscella rintelii

Fungal Planet 831 – 14 December 2018

Leptodiscella rintelii Hern.-Restr., *sp. nov.*

Etymology. *rintelii*, refers to the name of the collector of the ex-type strain, Marinus Rintel. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Muyocopronaceae*, *Muyocopronales*, *Dothideomycetes.*

Mycelium hyaline to pale brown composed of smooth-walled, septate, 1–2 µm wide hyphae. *Conidiophores* micro- to semi-micronematous composed of one to many globose to irregular cells, thin-walled, hyaline, smooth. *Conidiogenous cells* mono- or polyblastic, lateral or terminal, subcylindrical, globose or irregular, non-denticulate, hyaline, smooth, 3.5–6.5 × 3.5–5 µm. *Conidia* solitary, cylindrical, rounded at both ends or truncate base, hyaline, 1-septate, smooth, multi-guttulate, 8–14.5 × 3–4 µm, with a simple, filamentous subterminal appendage at each end, 2.5–6 µm long. *Chlamydospores* not observed.

Culture characteristics — Colonies on OA and CMA after 1 wk at 25 °C, aerial mycelium lacking except in the centre, where occasionally white tufts are observed, pale ochreous to cinnamon with age, reverse concolourous.

Typus. The Netherlands, Noord-Holland, Langedijk, Zuid-Scharwoude, isolated from soil, 2017, *M. Rintel* (holotype CBS H-23742, cultures ex-type CBS 144927 = JW174006, ITS and LSU sequences GenBank LR025180 and LR025181, MycoBank MB828022).

Notes — *Leptodiscella* is an uncommon genus known mainly from soil (Papendorf 1967, Matsushima 1975, Madrid et al. 2012) and dust (Udagawa & Toyazaki 1985). *Leptodiscella rintelii* is more similar to *L. africana* in having hyaline, 1-septate conidia and lacking chlamydospores (Papendorf 1967). However, *L. rintelii* can be distinguished from *L. africana* by having shorter and wider conidia with shorter appendages (11–17.5 × 2–3 µm, 6.5–13 µm long, in *L. africana*, Papendorf 1975).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *L. brevicatenata* (GenBank FR821312.1; Identities = 485/455 (96 %), 7 gaps (1 %)), *L. chlamydospora* (GenBank FR745398.1; Identities = 449/489 (92 %), 12 gaps (2 %)) and *L. africana* (GenBank NR_145359.1; Identities = 457/509 (90 %), 14 gaps (2 %)).

Colour illustrations. Garden where the soil sample was collected; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Parasarocladium debruynii

Fungal Planet 832 – 14 December 2018

Sarocladiaceae L. Lombard, *fam. nov.*

Classification — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes*.

Vegetative hyphae septate, hyaline, smooth- and thin-walled. *Conidiophores* erect, arising directly from vegetative hyphae, simple or branched, straight, hyaline, smooth-walled, aseptate or with basal septum. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monophialidic, aseptate, elongate-ampulliform to subcylindrical, thin- and smooth-walled, hyaline with inconspicuous collarettes and periclinal thickening; adelophialides and schizophialides present or absent. *Conidia* unicellular, ellipsoidal, bacilliform to fusiform, sometimes slightly curved, hyaline to subhyaline, thin- and smooth-walled, forming slimy heads on the phialides or produced in chains.

Type genus. *Sarocladium* W. Gams & D. Hawksw.
MycoBank MB828245

Notes — The family *Sarocladiaceae* presently includes *Parasarocladium* and *Sarocladium*.

Parasarocladium debruynii L. Lombard, *sp. nov*.

Etymology. Named for Remco de Bruyn, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Colonies on OA at 25 °C attaining 45–55 mm in 7 d, salmon due to abundant sporulation on medium surface giving a wet and slimy appearance, effuse, with edge entire surrounded by a light cyan blue halo; reverse salmon. On MEA at 25 °C attaining 38–50 mm in 7 d, rosy buff, effuse, with strong folds into the medium with edge entire; reverse rosy buff. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae, simple or rarely branched, straight, hyaline, smooth-walled, aseptate or with basal septum, up to 75 µm long. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monophialidic, aseptate, elongate-ampulliform to subcylindrical, 13–27 µm long, 1–3 µm wide at the base, thin- and smooth-walled, hyaline with inconspicuous collarettes and periclinal thickening. *Conidia* unicellular, ellipsoidal, bacilliform to fusiform, sometimes slightly curved, 3–5 × 1–2 µm (av. 4 × 2 µm), hyaline, thin- and smooth-walled, forming slimy heads on the phialides. *Chlamydospores* not seen.

Typus. The Netherlands, Utrecht, IJsselstein, from soil, Mar. 2017, *R. de Bruyn* (holotype CBS H-23746, culture ex-type CBS 144942 = JW180016; ITS, LSU, *tef1* and *tub2* sequences GenBank MK069420, MK069416, MK069410 and MK069407, MycoBank MB828217).

Notes — The genus *Parasarocladium* was recently introduced by Summerbell et al. (2018) and included three species, *P. breve*, *P. gamsii* and *P. radiatum*. Conidia of *P. debruynii* (3–5 × 1–2 µm) are smooth-walled compared to the chromophilic roughened conidia of *P. breve* (Gams 1971) and smaller than those of *P. gamsii* ((4–)5–7(–12) × 0.5–1 µm; Tichelaar 1972). Furthermore, the phialides of *P. debruynii* lack any septation, distinguishing it from *P. radiatum* (Gams 1971). Additionally, ribosomal DNA sequences resolved *P. debruynii* as a distinct lineage within the genus *Parasarocladium*.

Colour illustrations. Background, collection site (backyard); conidiophores and conidia. Scale bars = 10 µm.

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Conioscypha boutwelliae

Fungal Planet 833 – 14 December 2018

Conioscypha boutwelliae Hern.-Restr., *sp. nov.*

Etymology. *boutwelliae*, refers to the name of the collector of the ex-type strain, Katrina Boutwell. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Conioscyphaceae*, *Conioscyphales*, *Sordariomycetes.*

Description on OA. *Mycelium* composed of septate, hyaline, smooth, 1–2.5(–4) µm wide hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, cupulate, endogenous, multilayer cup-like collarette after several percurrent enteroblastic tiny elongations, hyaline, smooth, 11.5–20.5 × 8–15 µm. *Conidia* solitary, unicellular, ellipsoidal, obovoid or subglobose, base truncate with a central pore of 1–1.5 µm diam, brown, pitted-wall, 10.5–21 × 8–13.5 µm.

Culture characteristics — Colonies on OA after 1 wk at 25 °C, flat, spreading with scarce aerial mycelium, powdery, shiny, black, margin effuse.

Typus. The Netherlands, Zuid-Holland, Alphen aan den Rijn, isolated from soil, 2017, *K. Boutwell* (holotype CBS H-23743, cultures ex-type CBS 144928 = JW203008, ITS and LSU sequences GenBank LR025182 and LR025183, MycoBank MB828023).

Notes — *Conioscypha* includes 13 species mainly isolated as saprobes from submerged dead wood and leaves (Matsushima 1975, 1993, 1996, Shearer 1973, Crous et al. 2014a, Zelski et al. 2015, Chuaseeharonnachai et al. 2017, Hernández-Restrepo et al. 2017). *Conioscypha boutwelliae* is the first species described from soil, besides *C. varia* that has been reported from agricultural soil according to the CBS database. *Conioscypha boutwelliae* is similar to *C. japonica*, *C. lignicola* and *C. pleiomorpha* in having dark brown pitted conidia. However, they differ in shape and size, while in *C. boutwelliae* conidia are wider (8–13.5 µm) than in *C. japonica* (4.5–10 µm) and *C. pleiomorpha* (6–9 µm), they are narrower than in *C. lignicola* (11–12 µm).

Colour illustrations. Garden where the soil sample was collected; conidiogenous cells and conidia. Scale bars = 10 µm.

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Sarocladium dejongiae

Fungal Planet 834 – 14 December 2018

Sarocladium dejongiae L. Lombard, *sp. nov*.

Etymology. Named for Astrid de Jong, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes*.

Colonies on OA at 25 °C attaining 27–32 mm in 14 d, pale saffron to rosy buff, effuse, glabrous with undulate to lobate margin. On PDA at 25 °C attaining 38–43 mm in 14 d, saffron to salmon, effuse, glabrous, with edge entire. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae or from ropes of hyphae, simple or rarely branched, straight, hyaline, smooth-walled, up to 35 µm long. *Phialides* subcylindrical, 17–24 µm long, 1–2 µm wide at the base, thin- and smooth-walled, hyaline with inconspicuous periclinal thickening; adelophialides and schizophialides not observed. *Conidia* unicellular, cylindrical, ellipsoidal, ovoid to irregular, 3–5 × 1–2 µm (av. 3 × 1.5 µm), hyaline, thin- and smooth-walled, arranged in slimy heads. *Chlamydospores* rare, intercalarily, smooth-walled, 5 µm diam.

Typus. The Netherlands, Friesland, Jowert, from soil, Mar. 2017, *A. de Jong* (holotype CBS H-23744, culture ex-type CBS 144929 = JW244007; ITS, LSU, *tef1* and *tub2* sequences GenBank MK069419, MK069415, MK069409 and MK069406, MycoBank MB828218).

Notes — *Sarocladium dejongii* is morphologically similar to several species characterised by producing conidia in slimy heads (Giraldo et al. 2015). However, this species is distinguished from all these species by the multiple conidial shapes produced and the formation of intercalary chlamydospores. Additionally, ribosomal DNA sequences resolved *S. dejongiae* as a distinct lineage within the genus *Sarocladium*.

Colour illustrations. Background, collection site (backyard); colonies on OA and PDA, conidiophores with slimy heads, conidia and chlamydospores. Scale bars = 10 µm.

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Lectera nordwiniana
nordwin
COLLEGE

Fungal Planet 835 – 14 December 2018

Lectera nordwiniana Giraldo López, *sp. nov.*

Etymology. *nordwiniana*, refers to the school named 'Nordwin College' where the soil sample was collected by the students Dylan van der Pol, Rémon Verf, Joost Wilks and Mathis de Ruiter. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes.*

Mycelium consisting of branched, septate, smooth, hyaline and thin-walled hyphae, up to 2 µm wide. *Conidiomata* sporodochial, punctiform, dark brown, solitary or gregarious, surrounded by abundant setae. *Setae* dark brown, 3–8-septate, flexuous, tapering to acutely rounded apices, thick- and smooth-walled, intermingled among the conidiogenous cells, 78–193 × 3–5 µm. *Phialides* subcylindrical, hyaline, smooth-walled, 13–24.5 µm long, 1.5–2.5 µm wide at the base, with conspicuous periclinal thickening at the conidiogenous locus. *Conidia* broadly fusiform, acute ends, inequilateral, with inner plane flat, and outer plane convex, 1-celled, hyaline, becoming orange in mass, thick- and smooth-walled, 6–8 × 2–3 µm.

Culture characteristics — Colonies on PDA after 14 d at c. 25 °C, reaching 22–23 mm diam, elevated, slightly folded, salmon, with brown punctiform sporodochia on the top.

Typus. The Netherlands, Friesland, Leeuwarden, Nordwin College, from soil, 2017, coll. *D. van der Pol*, *R. Verf*, *J. Wilks* & *M. de Ruiter*, isol. *A. Giraldo* (holotype CBS H-23736, cultures ex-type CBS 144921 = JW231009, ITS, LSU, *tef1*-α and *rpb2* sequences GenBank MK047461.1, MK047511.1, MK047549.1 and MK047570.1, MycoBank MB828024).

Additional materials examined. The Netherlands, Friesland, Leeuwarden, Nordwin College, from soil, 2017, coll. *D. van der Pol*, *R. Verf*, *J. Wilks* & *M. de Ruiter*, isol. *A. Giraldo*, JW231013, ITS, LSU, *tef1*-α and *rpb2* sequences GenBank MK047462.1, MK047512.1, MK047550.1 and MK047571.1; Gelderland, Arnhem, from soil, 2017, coll. *J.* & *L. Visser*, isol. *A. Giraldo*, CBS 144922 = JW 46012, ITS, LSU, *tef1*-α and *rpb2* sequences GenBank MK047463.1, MK047513.1, MK047551.1 and MK047572.1.

Notes — *Lectera* was introduced based on the plant pathogen *Lectera colletotrichoides* as the type species, along with *L. longa* (Cannon et al. 2012). Recently, three more species have been added to the genus, i.e., *Lectera capsica* from *Capsicum annuum*, *L. phaseola* from *Phaseolus vulgaris* and *L. humicola* from soil (Crous et al. 2017a, Giraldo & Crous, in prep.). Morphologically, *L. nordwiniana* resembles *L. longa* and *L. phaseola* in the profuse production of flexuous setae in artificial media. However, in *L. nordwiniana* these structures are longer (up to 193 µm long) than those produced by the other species (*L. longa* up to 111 µm long, *L. phaseola* up to 38 µm long).

Colour illustrations. Netherlands, Nordwin College where the soil sample was collected; sporodochium, setae, conidiogenous cell and conidia. Scale bars = 10 µm.

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Clathrus natalensis

Fungal Planet 836 – 14 December 2018

Clathrus natalensis G.S. Medeiros, Melanda, T.S. Cabral, B.D.B Silva & Baseia, *sp. nov.*

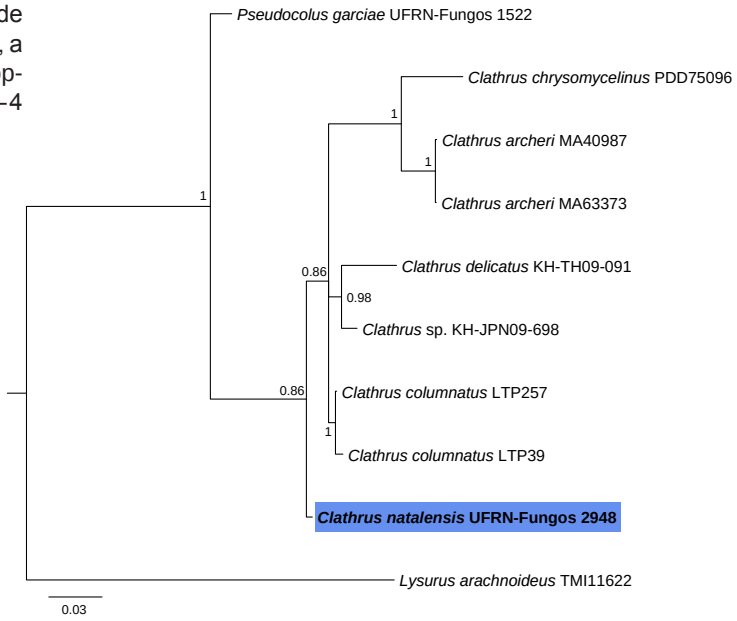
Etymology. Named in reference to the type locality, Natal City.

Classification — *Clathraceae*, *Phallales*, *Phallomycetidae*.

Immature *basidiomata* subglobose, 13–18 × 16–22 mm, greyish white (12A1–12B1 KW) with a single and thick rhizomorph greyish white (12A1–12B1 KW). Expanded basidiomata obovate to subglobose 46–95 × 24–71 mm. *Arm meshes* pentagonal to hexagonal, rugose at the beginning of development, becoming smooth afterwards, 32–90 × 20–70 mm, dull red to pinkish white (8B3–8A2), transverse section of an arm shows 3–4 tubes subglobose, elongated to piriform. *Pseudostipe* absent. *Gleba* mucilaginous, in all inner part of arms, olive brown (KW 4F4), with an unpleasant smell. *Volva* 50–140 × 10–40 mm, greyish white (12A1–12B1 KW), with thick rhizomorph, greyish white (12A1–12B1 KW). *Basidiospores* cylindrical, 4.6–5.6 × 1.9–2.7 µm (5.2 ± 0.4 × 2.3 ± 0.3 µm; Qm = 2.29; n = 30 spores), wall ≤ 0.7 µm, smooth, hyaline in KOH. Arms exhibiting subglobose to globose and pyriform cells, 19.5–45.6 × 13–33.5 µm, wall ≤ 2.2 µm diam, hyaline. *Volva* composed of filamentous hyphae, 2.7–5.2 µm diam, wall ≤ 1.1 µm diam. *Rhizomorph* composed of filamentous hyphae, 3.2–4.7 µm diam, wall ≤ 0.9 µm diam.

Typus. Brazil, Rio Grande do Norte, Natal, Centro de Biociências, on soil with litter, 5 Apr. 2017, *G.S. Medeiros* (holotype UFRN-Fungos 2948, isotype UFRN-Fungos 2947, paratype UFRN-Fungos 2946, ITS and LSU sequences GenBank MH107232 and MH107235, MycoBank MB824737).

Notes — *Clathrus natalensis* was found in a remnant of Atlantic rainforest at the Universidade Federal do Rio Grande do Norte (UFRN) and is characterised by robust basidiomata, a pale red colouration, rugose arms at the beginning of development, becoming smooth afterwards, with the presence of 3–4 tubes in transverse section. This species presents similarities with *Clathrus cristatus* with the colour of the arms and mesh arrangement, but that presents basidiomata with crests along the arm edges (Fazolino et al. 2010), a characteristic absent in *C. natalensis.* In a BLASTn search, the ITS sequence obtained in this study has 94 % similarity to *Clathrus ruber* (GenBank GQ981501). However, *C. ruber* can easily be distinguished by the bright red colour, smaller meshes, and the immature basidiome marked by reticulations (Dring 1980). In the phylogenetic analysis, *C. natalensis* does not group with any species available on GenBank; in fact, they are clearly morphologically different. *Clathrus columnatus* and *C. archeri* show distinct receptacle arrangements, columnar in the first, and united arms below with pointed tips initially attached in the latter (Bosc 1811, Dring 1980); *C. crysomycelinus* and *C. delicatus* have white basidiomata, the first differs by a glebifer attached at the junction of the arms, and the second by a smaller receptacle (up to 25 mm high × 15 mm wide) and deep grooves in the outer face of the arms (Möller 1895, Dring 1980) – characteristics absent in *C. natalensis.* Thus, both morphological characters and the phylogenetic analysis separate *C. natalensis* from the already known species.



Phylogenetic tree obtained with MrBayes v. 3.1.2. (Huelsenbeck & Ronquist 2001) using ITS, nuc-LSU and *atp6* (MK035869), under GTR+G (ITS/nucLSU) and HKY+G models (*atp6*), for 20 M generations. The type specimen is marked with a rectangle. Posterior probability values are indicated on the branches. TreeBASE submission ID 22520.

Colour illustrations. Brazil, Universidade Federal do Rio Grande do Norte, Centro de Biociências, locality where the type species was collected; basidiomata, transverse section of an arm showing the tubes, subglobose to globose and pyriform cells on arm, smooth spores, and filamentous hyphae in the rhizomorph. Scale bars = 20 mm (basidiomata), 2 mm (tubes), 10 µm (cells on arm, spores and rhizomorph hyphae). All morphology photos from the holotype UFRN-Fungos 2948.

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Colletotrichum arboricola

Fungal Planet 837 – 14 December 2018

Colletotrichum arboricola M. Zapata, M.A. Palma & Piont., *sp. nov.*

Etymology. The epithet refers to being a tree inhabitant.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

Sexual morph on Anthriscus stem (microscopic preparations in 60 % lactic acid, with 50 measurements per structure). *Ascomata* globose to pyriforme, glabrous to slightly pilose, medium brown to uniformly darker. *Peridium* 8–13 µm thick, composed of brown flattened angular cells, 6–14 µm diam. *Ascogenous hyphae* hyaline, smooth-walled, delicate. *Interascal tissue* composed of fine paraphyses with scarce septa, more apparent in immature perithecia, arranged in irregular masses of hyaline filament with round tips, 35–85 × 1–2 µm. *Asci* cylindrical, unitunicate, 8-spored, 67–86 × 8–13 µm. *Ascospores* uni- to biseriate, aseptate, hyaline, smooth-walled, with both ends round, sometime slightly curved, (12–)13–16(–17) × (3.5–)4–5.3(–6) µm, mean ± SD 14.3 ± 1.1 × 4.4 ± 0.5, L/W ratio 3.2.

Asexual morph on SNA. *Vegetative hyphae* 1.5–7 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Clamydospores* not observed. *Setae* not observed or rare. *Conidiomata* absent, conidiophores formed directly from vegetative hyphae, simple or septate and frequently branched, 14–41 µm long. *Conidiogenous cells* hyaline, smooth-walled cylindrical to ampulliform, sometimes integrated (not separated from fertile hyphae by a septum), polyphialides rarely observed, phialides measuring 10–22 × 1.8–3.3 µm, opening 1–1.5 µm diam, collarette not visible or ≤ 0.3 µm long, periclinal thickening not observed or rare. *Conidia* hyaline, smooth-walled, aseptate, mainly straight, sometimes slightly constricted in the middle, cylindrical, with one end rounded and the other slightly acute to truncate with cytoplasm little granular, (16.2–)17.1–20(–23.3) × (4.8–)5–5.6(–5.9) µm, mean ± SD 18.6 ± 1.4 × 5.4 ± 0.2 µm, L/W ratio = 3.5. *Appressoria* single, solitary, brown, smooth-walled, clavate to elliptical, the edge entirely or slightly undulated, (6.9–)7.6–12.4(–16.9) × (3–)4.1–6.3(–6.9) µm, mean ± SD 9.6 ± 2.1 × 5.1 ± 0.9 µm, L/W ratio = 2 (more abundant in oat meal agar).

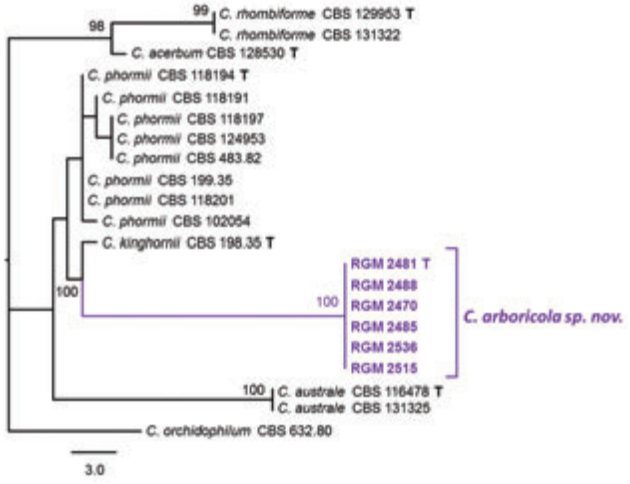
Asexual morph on Anthriscus stem. Conidiomata absent. *Setae* not observed. *Conidiophores* formed directly on hyphae, abundant, hyaline, smooth-walled, sometimes septate, branched, to 35 µm long. *Conidiogenous cell* hyaline, smooth-walled, cylindrical to clavate 9–16.5 × 2–4 µm, opening 1–1.5 µm, collarette ≤ 0.5 µm long or not visible, periclinal thickening not observed or rare. *Conidia* hyaline, smooth-walled, aseptate (sometimes with a septum before germination), straight to slightly curved, cylindrical, with one end round and other end sometimes slightly acute, (15.7–)16.7–19.2(–20.3) × (4.4–)4.9–5.3(–5.6) µm, mean ± SD 17.9 ± 1 × 5.1 ± 0.2 µm, L/W ratio = 3.5.

Culture characteristics — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to pale olivaceous grey, with low white aerial mycelium, filter paper and *Anthriscus* stem partly covered with grey fruiting bodies (ascomata), reaching 58.8 ± 1.4 mm diam. Colonies on OA flat with entire margin, with felty or short floccose olivaceous grey aerial mycelium, reaching 65.6 ± 1 mm diam. *Conidia in mass* salmon.

Typus. Chile, Los Ángeles, on leaves of *Fuchsia magellanica* (*Onagraceae*), 11 July 2012, *J. Jure* (holotype RGM 2481, culture ex-type SAG 53350-12 = CBS 144795; ITS, LSU, *GAPDH*, *ACT* and *TUB2* sequences GenBank MH817944, MK014743, MH817950, MH817956 and MH817962, MycoBank MB827627, TreeBASE Submission ID 23265).

For additional material examined, see MycoBank.

Notes — *Colletotrichum arboricola* was isolated for the first time on leaves of *Fuchsia magellanica*, but its presence has since been observed in different arboreal hosts in the central area of Chile. A phylogenetic analysis based on sequence data from four loci (ITS, *GAPDH*, *ACT* and *TUB2*) places the fungus in clade 5 of the *Colletotrichum acutatum* complex (Damm et al. 2012). *Colletotrichum arboricola* is separated from other species by *GAPDH* and *ACT*, with *GAPDH* performing best as a diagnostic sequence. The closest matches in a BLASTn searches with the *GAPDH* sequence were *C. phormii* CBS 118194 (GenBank JQ948777; Identities = 245/252 (97 %), no gaps), *C. acerbum* CBS 128530 (GenBank JQ948790; Identities = 242/252 (96 %), no gaps) and *C. johnstonii* CBS 128532 (GenBank JQ948775; Identities = 241/252 (96 %), no gaps). Due to size and shape overlapping of conidia, appressoria and ascospores with others members of the complex, *C. arboricola* is not reliably distinguishable using morphological characteristics.



One of the two equally most parsimonious trees (67 steps, CI = 0.896, HI = 0.104, RI = 0.957) obtained from the multilocus phylogenetic analysis (ITS-*GAPDH*-*ACT*-*TUB2*) for selected *Colletotrichum* species belonging to the *C. acutatum* complex. The analysis was conducted with PAUP v. 4.0b10 (Swofford 2003). DNA sequences were aligned using MAFFT v. 7.0 employing the E-INS-i strategy. Bootstrap support values ≥ 75 % are shown above nodes (1 000 replicates). The tree was rooted with *Colletotrichum orchidophilum*. T = ex-type.

Colour illustrations. Fuchsia magellanica growing in natural habitats of Chile (courtesy Fernan Silva 2017); asci, ascospores and conidiophores on *Anthriscus* stem (in lactophenol-cotton-blue), appressoria and conidia. Scale bars = 10 µm.

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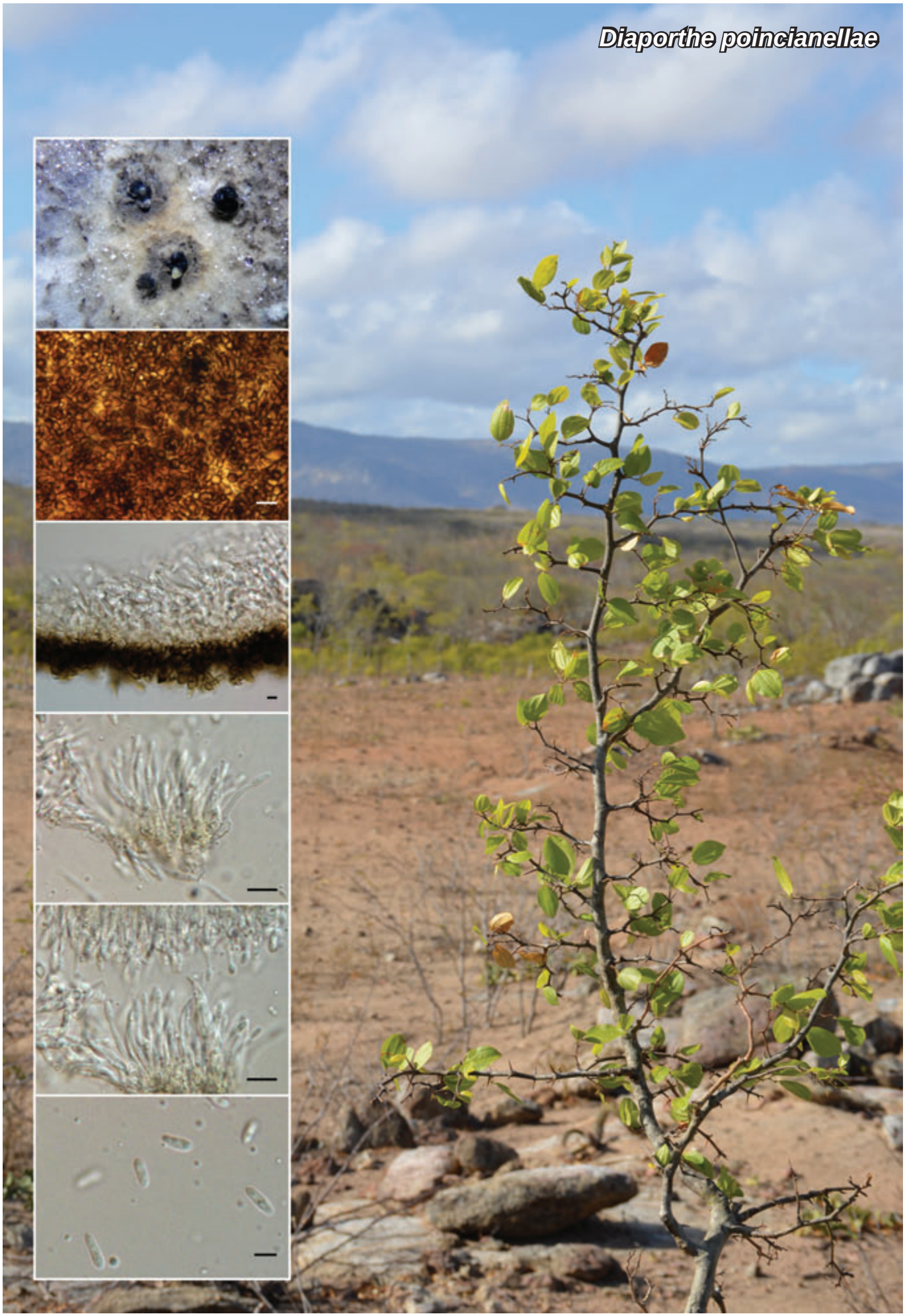

Diaporthe poincianellae

Fungal Planet 838 – 14 December 2018

Diaporthe poincianellae T.G.L Oliveira, O.M.C. Magalhães & J.D.P. Bezerra, *sp. nov.*

Etymology. Name refers to *Poincianella*, the host plant genus from which it was isolated.

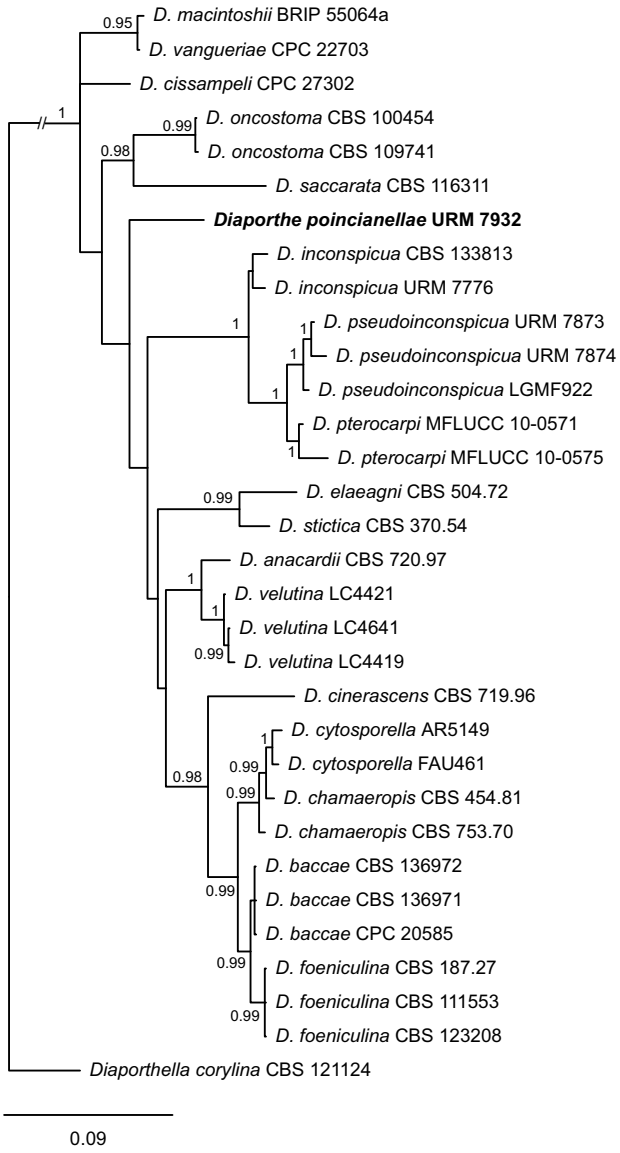
Classification — *Diaporthaceae*, *Diaporthales*, *Sordariomycetes*.

Conidiomata pycnidial in culture, globose to subglobose with thin wall, solitary or aggregated, dark brown to black, (212–)265–350 × (180–)265–318 µm, with cream to yellowish conidial drops exuding from the ostioles. *Conidiogenous cells* phialidic, hyaline, occasionally branched, straight to sinuous, slightly tapering towards the apex and slightly curved, 10.5–12.5 × 2–2.2 µm. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid to ellipsoidal, slightly tapered towards the rounded end, truncated base, 5.5–7.5(–8.5) × 3–3.5 µm. *Beta conidia* not observed. *Sexual morph* not observed.

Culture characteristics — On PDA at 25 °C in darkness, 8 cm diam after 15 d, colony initially white greyish, becoming yellowish, fluffy and whitish aerial mycelium. Reverse dark brown to black. Pycnidia forming after 15 d. On MEA at 25 °C in darkness, colony initially white to greyish, becoming yellowish, fluffy and whitish aerial mycelium, with slow growth reaching 5.5 cm diam after 15 d. Reverse dark brown to black with small whitish parts. Pycnidia forming after 15 d.

Typus. Brazil, Paraíba state, Santa Teresinha, Tamanduá farm (S07°1.524 W037°23.518), as endophyte from branches of *Poincianella pyramidalis* (*Fabaceae*), May 2013, *J.D.P. Bezerra* (holotype URM 91976, culture extype URM 7932, ITS, LSU, *CaM*, *his3*, *tef1-α* and *tub2* sequences GenBank MH989509, MH989513, MH989540, MH989539, MH989538 and MH989537, MycoBank MB827977).

Notes — The genus *Diaporthe* has been extensively reviewed and several new species have been included in it (Marin-Felix et al. 2019). BLASTn searches using ITS sequence of *Diaporthe poincianellae* demonstrated 99 % similarity to *D. velutina* (GenBank NR_152470.1), amongst others. The LSU sequence is 99 % similar to *D. phragmitis* (GenBank MH878644.1), amongst others. The *CaM* sequence has 93 % similarity to *D. anacardii* (GenBank KC343266.1). The *his3* sequence is 94 % similarity to *D. inconspicua* and *D. pseudoinconspicua* (e.g., GenBank KC343607.1 and MH122517.1). Based on the *tef1* sequence *D. poincianellae* is 88 % similarity to *D. velutina* (GenBank KX999178.1), and based on *tub2* sequence it is 95 % similar to *D. cissampeli* (GenBank KX228384.1). Morphologically, *D. poincianellae* differs from *D. velutina* based on the size of pycnidia (69–428 µm diam), conidiophores (10–23 × 1–2.5 µm), alpha conidia sometimes clavate (5.5–10 × 2–2.5 µm) and by the presence of beta conidia (Gao et al. 2017). Furthermore, *D. poincianellae* also differs from *D. cissampeli* by the size of its pycnidia (up to 200 µm diam), conidiogenous cells phialidic (10–15 × 1–2 µm) and alpha conidia subcylindrical (7.5–12 × 2–3 µm) (Crous et al. 2016b).



Bayesian inference tree obtained by a phylogenetic analysis of the combined ITS rDNA, *tef1-α* and *tub2* sequences conducted in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The substitution model K80+I+G was used for ITS and HKY+G for *tef1-α* and *tub2* alignments. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold** face. *Diaporthella corylina* (CBS 121124) was used as outgroup.

Colour illustrations. Brazilian tropical dry forest; conidiomata pycnidial; alpha conidiophores and conidia. Scale bars = 10 µm.

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Entoloma silvae-frondosae

Fungal Planet 839 – 14 December 2018

Entoloma silvae-frondosae Dima, O.V. Morozova, Noordel., Brandrud & Krisai, *sp. nov*.

Etymology. The epithet refers to the habitat of the species in broad-leaved forests.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid to tricholomatoid. *Pileus* 11–50 mm diam, initially hemispherical to convex with or without a small acute umbo, becoming applanate with central depression, with involute then straight margin, hygrophanous, translucently striate at margin when expanded, quickly pallescent on drying, when moist initially pale brownish grey to ochraceous grey, becoming paler, whitish grey (3B3–4, 4B3–4, 4C3–4, 5B3–4, 6D5–6, Kornerup & Wanscher 1978), often almost white when dry (4A2), surface dry, smooth, glabrous, sometimes with a few scattered, white hairs at margin (when young and fresh). *Lamellae* moderately distant (L = 30–40, l = 1–3), adnexed, adnate-emarginate or adnate with small tooth, arcuate-segmentiform, narrow, whitish, pale grey, becoming pinkish or orange-white (5A2, 6A2), with entire, concolorous edge. *Stipe* 30–80 × 3–7 mm, cylindrical or fusiform, base rarely broadened, sometimes tapering towards base, white, greyish pale to watery grey, longitudinally fibrillose striate, base distinctly hairy. *Context* greyish beige, hygrophanous, solid then hollow. *Smell* nitrous or somewhat soap-like, or with a sweetish, perfume-component, somewhat farinaceous. *Spores* (7–)8–9.5(–12) × (5.5–)6–8(–9) µm, Q = (1–)1.2–1.3(–1.5), subisodiametrical, with 5–7 angles in side-view. *Basidia* 28–45 × 8–11 µm, 4-spored, narrowly clavate to clavate. *Cheilocystidia* absent. *Hymenophoral trama* regular, made up of inflated elements, 55–130 × 6–13 µm. *Pileipellis* a cutis of parallel, cylindrical hyphae, 3–7 µm wide, with slender clavate terminal elements up to 12 µm wide, these a bit uplifted; subpellis well-differentiated, made up of inflated elements, 40–100 × 8–28 µm. *Pileitrama* regular, made up of inflated elements, 45–120 × 20–35 µm. *Pigment* intracellular and sometimes with additionally incrusted thin hyphae of pileipellis. *Clamp-connections* abundant in all structures.

Habit, Habitat & Distribution — In groups on soil in broad-leaved forests, mainly under *Carpinus*, *Quercus*, *Fagus* or *Tilia*. Known from Austria, Estonia, Hungary, Norway, Russian Caucasus, and Iran (from root samples).

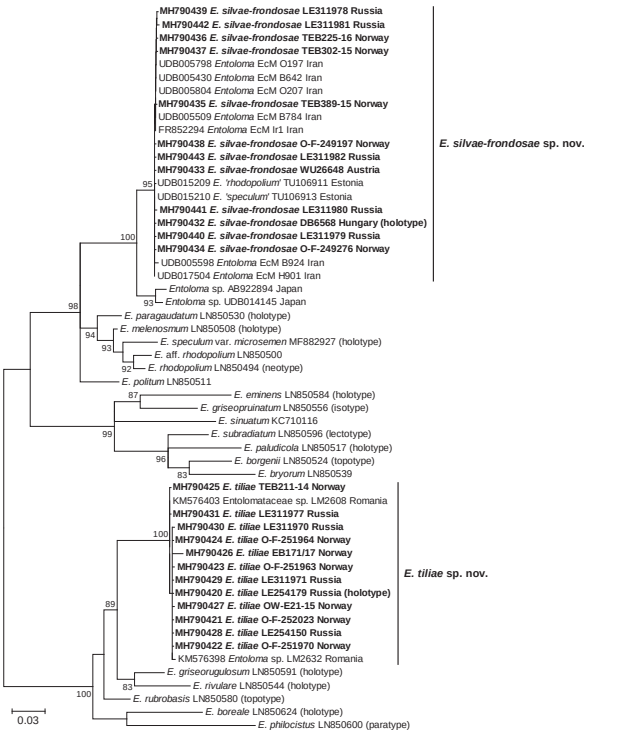
Typus. Hungary, Vas, Apátistvánfalva, N46.888488° E16.261684°, in *Carpinus betulus-Pinus sylvestris* mixed forest, 30 Sept. 2017, *B. Dima & L. Albert*, DB6568 (holotype L, isotypes BP, O, ITS and LSU sequences GenBank MH790432 and MH792065, MycoBank MB827526).

For additional material examined, see MycoBank.

Notes — *Entoloma silvae-frondosae* is nested within the *E. rhodopolium* s.str. group, which is characterised by rather pale basidiomata, often developing a slightly clitocyboid habit with depressed pileus centre, with a hygrophanous, often translucently striate pileus, a relatively fragile white stipe, isodiametrical or subisodiametrical spores, and a nitrous (to soap-like) smell. The smell of the species in the *E. rhodopolium-E. nidorosum* group is rather variable, and perceived differently by different mycologist, but it is definitely different from the pure and often strong farinaceous smell and taste found in other rhodopolioid *Entoloma* species.

Diagnostic features of *E. silvae-frondosae* are pale basidiomata with distinctly hairy stipe base, and occurrence in temperate broad-leaved forests with *Carpinus*, *Fagus* and *Tilia*. Similar species within the *E. rhodopolium* clade, such as *E. melenosmum* (= *E. nidorosum*, Kokkonen 2015), *E. nidorosum* and *E. politum*, have another ecology, preferring moist to swampy *Betula* and *Salix* forests. In addition, they usually have darker basidiomata. However, *E. rhodopolium* s.str. often grows in similar habitat as *E. silvae-frondosae* like *Corylus* and *Fagus* forests in boreonemoral-temperate regions (Kokkonen 2015, Brandrud et al. 2018). Although *E. rhodopolium* s.str. has on average somewhat darker, larger basidiomata with less distinct hairy stipe base, it might sometimes be difficult to distinguish it morphologically from *E. silvae-frondosae*.

For supplementary information see MycoBank



Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values shown at the nodes (BS > 80 %). Sequences of the new species generated for this study in **bold** face.

Colour illustrations. Russia, Krasnodar Territory, Adler District, Aibga forestry, valley of the Bezymyannaya River, flood-plain forest; spores, pileipellis (all from holotype DB6568), basidiomata *in situ* (LE311980), hairs at stipe base of the basidioma from LE311981, basidiomata *in situ* (holotype DB6568). Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

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Entoloma tiliae

Fungal Planet 840 – 14 December 2018

Entoloma tiliae Brandrud, O.V. Morozova, Dima, Bendiksen & Noordel., *sp. nov*.

Etymology. The epithet refers to the occurrence of the species with *Tilia* spp., in calcareous *Tilia* forests and parks with *Tilia*.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, tricholomatoid. *Pileus* 20–60 mm diam, initially hemispherical-campanulate to convex-umbonate, becoming applanate with or without a low and broad central umbo, with slightly involute then straight margin, typically strongly hygrophanous, in exposed habitats often only seen in dried up state, and then rather pale brownish grey, in shadow rich places in water-soaked state starting off rather dark greyish brown to greyish brown (6F4–6, 7F3–6, Kornerup & Wanscher 1978), sometimes almost black at centre or the entire pileus when young, pallescent when drying up to pale brownish but small or expanded, thin-fleshed basidiomata can be much paler when dry grey (5D4–6, 5E4–6 up to 5C3–4); surface dry, glabrous, smooth or slightly rugose in the centre, initially sometimes finely white-silvery fibrillose-pruinose at centre, not striate when young, only weakly striate at margin when mature. *Lamellae* moderately distant (L = 30–40, l = 3–5), adnexed, adnate-emarginate or adnate with small decurrent tooth, whitish to pale greyish, becoming pinkish or greyish pink (7A2–3), with entire, concolorous edge. *Stipe* 30–70 × 3–11 mm, cylindrical or slightly fusiform, base sometimes tapered, sometimes distinctly clavate-bulbous (up to 1 cm broad) longitudinally fibrillose striate due to whitish fibrils on more or less greyish background, with age or when dry whitish; basal mycelium sparse, white, cottony, sometimes with white rhizomorphs; sometimes with reddish spots at the stipe base (also in context). *Context* greyish in the stipe and under the pileus surface, usually whitish in the inner part of the pileus, when dry whitish in most of context. *Smell* and *taste* farinaceous. *Spores* (8–)9–9.5(–11.5) × (6.5–)7–7.5(–9) µm, Q = (1–)1.2–1.3(–1.4), subisodiametrical, with 6–7 angles in side-view. *Basidia* 38–48 × 11–12.5 µm, 4-spored, narrowly clavate to clavate, clamped. *Cheilocystidia* absent. *Hymenophoral trama* regular, made up of inflated elements, 70–150 × 5–10 µm. *Pileipellis* a cutis with a transition to a trichoderm in the centre made up of cylindrical hyphae, 3–6 µm wide, with cylindrical to irregular terminal elements, sometimes differentiated as clavate to sphaeropedunculate cystidia-like elements up to 15 µm wide and 53 µm long; with brown intracellular pigment, often also with encrusted pigment in some narrow hyphae of pileipellis and subpellis. *Clamp-connections* abundant in all structures.

Habit, Habitat & Distribution — In groups on soil in calcareous *Tilia cordata* forests and parks with *Tilia* × *europaea* (= *T.* × *vulgaris*) and *T. cordata*. Known from SE Norway (Oslofjord area), Romania (environmental/soil sample) and European Russia (Saint Petersburg).

Typus. Russia, Saint Petersburg, Botanical Garden of the Komarov Botanical Institute RAS, N59.968889° E30.320833°, under *Tilia* × *europaea*, 19 Aug. 2011, *O. Morozova* (holotype LE254179, ITS and LSU sequences GenBank MH790420 and MH792063, MycoBank MB827527), as *E. gerriae* in Morozova et al. (2014).

For additional material examined, see MycoBank.

Notes — *Entoloma tiliae* is characterised by an usually uniformly dark-coloured pileus, longitudinally fibrillose striate rather rigid greyish stipe, isodiametrical or subisodiametrical spores, intracellular and additionally minutely incrusting pigments and a farinaceous smell. The majority of collections also exhibit some reddish spots/stains at bulb base on a few specimens. According to our phylogeny, the species belongs to a well-supported clade including, e.g., *E. rubrobasis* and *E. griseorugulosum* (Brandrud et al. 2018). In our phylogram, the species comes out as a sister to *E. griseorugulosum* and *E. rivulare*. *Entoloma griseorugulosum* has a resembling morphology and ecology, but it is distinguished on the rugulose pileus surface and habitat in the *Quercus* and *Castanea* forests. Furthermore, reddish stains at the base of the stipe is never noted on *E. griseorugulosum*. The recently described *E. rivulare* (Kokkonen 2015) is a small, boreal species, associated with wet habitats with *Alnus* or *Populus*. *Entoloma rubrobasis* (also demonstrating reddish tinge in the stipe base) and *E. boreale* are so far found only in Fennoscandian boreal coniferous forests, probably associated mainly with *Betula* and *Picea*, respectively (Kokkonen 2015, Brandrud et al. 2018).

Entoloma griseoluridum is another deciduous forest species described with somewhat similar features, but we have not been able to sequence the type of this species. According to the protologue (Kühner in Kühner & Romagnesi 1954), *E. griseoluridum*, however, lacks incrusting pigment on the narrow hyphae of pileipellis, it is more robust species with purplish red tinge in pileus, has dark lamellae, and it grows in *Quercus*, *Fagus*, *Carpinus* forests. Ludwig (2007) considered *E. griseopruinatum* and *E. griseoluridum* synonymous. *Entoloma gerriae*, also a very dark species from a similar habitat, differs by the more slender and tender basidiomata, coarsely incrusting and very dark intracellular pigment, and its holotype sequence nests in a distinct, rather distant clade. Some specimens of *Entoloma tiliae* previously were erroneously interpreted as *Entoloma griseoluridum* (e.g., in Zhukova et al. 2017), another deciduous forest species described with somewhat similar features. Unfortunately, we have not been able to sequence the type of this species.

See tree on Fungal Planet 839.

Colour illustrations. Russia, Saint Petersburg, Botanical Garden of the Komarov Botanical Institute RAS, park with planted *Tilia* × *europaea*, type locality; spores, hymenium, pileipellis near the pileus margin, pileipellis in the centre with pileocystidia (all from holotype), basidiomata in situ (LE254150), basidiomata in situ (holotype), longitudinal section of the basidioma from holotype. Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

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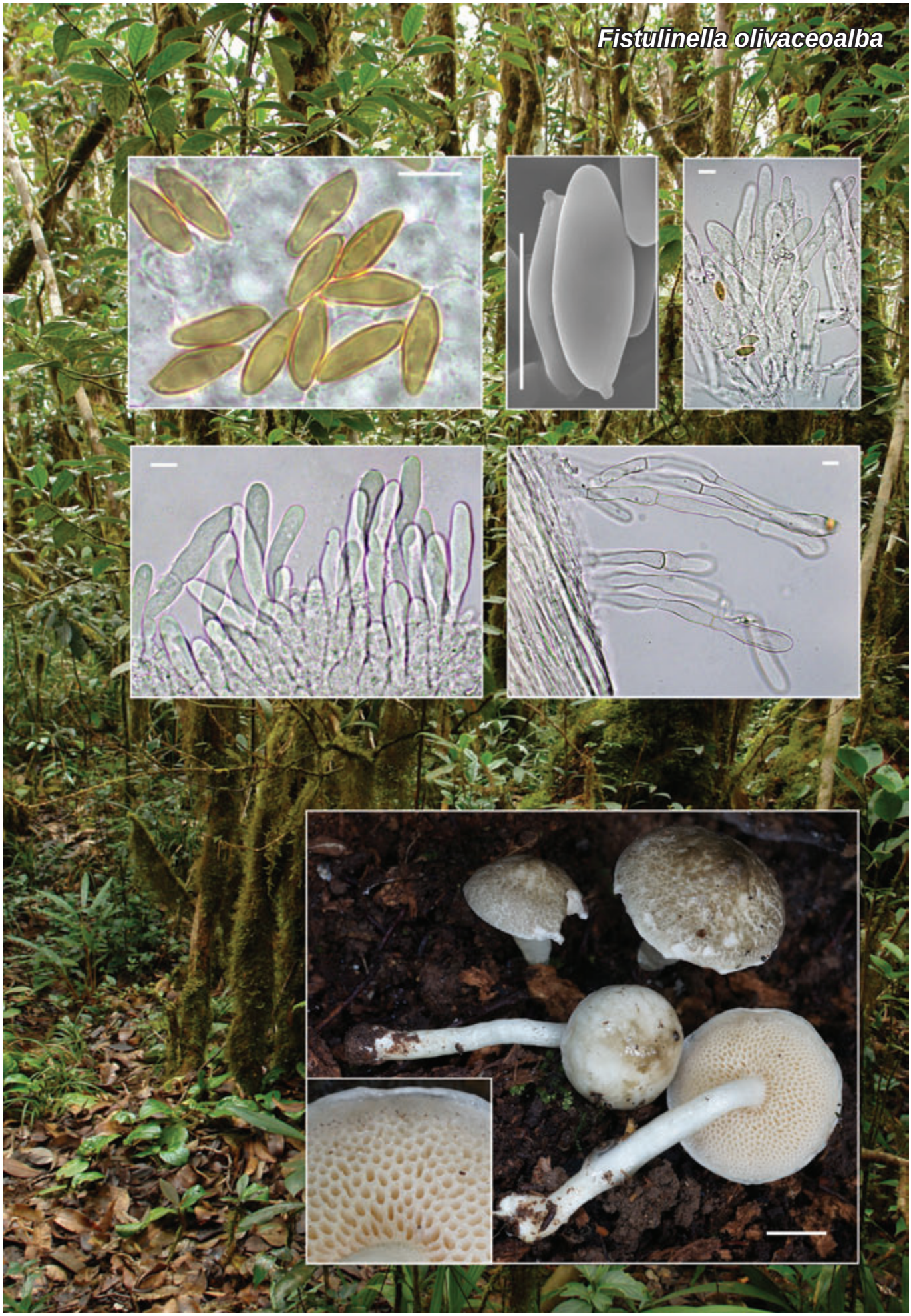
Fistulinella olivaceoalba

Fungal Planet 841 – 14 December 2018

Fistulinella olivaceoalba T.H.G. Pham, Y.C. Li & O.V. Morozova, *sp. nov*.

Etymology. The epithet refers to the white and olivaceous colours of the basidiomata.

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes*.

Basidiomata small to medium sized, boletoid. *Pileus* 15–50 mm diam, hemispherical to convex or subapplanate; with dark olivaceous grey (4D3–4, 4E3–5, 5D3–5E3, Kornerup & Wanscher 1978), greyish beige (4C3–4) to dark green, greyish green or olive green (28E8, 28C3–5, 30E7–8) scales and flakes over white background, becoming when mature grass green to yellowish green (30E7, 29B5–6), embedded in the gelatinous matter, more closely spaced in centre; slimy to viscid, in wet condition; margin almost lacking scales, white, overhanging the hymenophore, entire, slightly inrolled when young. *Hymenophore* tubular, adnate-emarginate to shortly decurrent with tooth to the stipe, 3–8 mm thick, whitish to creme (4A1–3), unchanging in colour when bruised, pinkish from spores in maturity; pores rounded to angular, 1–2/mm, with fringed edge; tubes concolorous with the hymenophore surface. *Spore print* brownish pink. *Stipe* 40–90 × 3–7 mm, cylindrical or slightly broader in the basal part, white, sparsely covered with dotted or granular scales (especially in the upper part) on white background, sometimes yellowish near the base, slimy to viscid. *Context* white, unchanging. *Smell* spicy, *taste* mild or sometimes bitter. *Basidiospores* (11–)13.5–14(–16.5) × (4–)4.5–5(–5.5) µm, Q = (2.5–)2.8(–3.3), fusoid, subfusoid and inequilateral in side view with weak suprahilar depression, narrowly oblong to subfusoid in ventral view, yellowish to brownish yellow in KOH, weakly dextrinoid, smooth. *Basidia* 22–37 × 8–11 µm, 4-spored, sometimes 2-spored, clavate. *Cheilocystidia* 55–130 × 8–18 µm, forming a sterile edge, septate, consist of 2–3 cells, cylindrical with broadened and sometimes rostrate terminal cells 25–41 × 5–9 µm, thin-walled. *Pleurocystidia* 35–75 × 5–10 µm, cylindrical, fusiform, subfusoid to narrowly lageniform, or subfusoid-mucronate to ventricose-mucronate, thin-walled, sparse. *Hymenophoral trama* divergent. *Pileipellis* an ixotrichoderm, made up of yellowish to brownish, cylindrical gelatinous interwoven hyphae 2.5–4 µm wide with narrowly clavate or fusiform terminal cells, 26–80 × 5–10 µm, pigment incrusting and additionally pale intracellular. *Pileal trama* composed of interwoven hyphae 3.5–5.5 µm wide. *Stipitipellis* a cutis of hyaline parallel hyphae, 2–5 µm wide. *Caulocystidia* 68–130 × 11–16 µm, as cylindrical, septate hairs with clavate or sometimes rostrate terminal cells. *Clamp connections* absent.

Habit, Habitat & Distribution — In groups on soil in tropical lowland and montane evergreen broadleaf forest. Known from Vietnam, China and Japan.

Typus. Vietnam, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba National Park, Hon Giao Ranger Station, path to Hon Giao Mt, N12.192222° E108.711111°, 1 850 m alt., upper montane mossy evergreen broadleaf forest, on soil and on the base of tree, 26 May 2014, *O. Morozova* (holotype, LE312004, *tef1α*, ITS and LSU sequences GenBank MH733592, MH718344 and MH718396, MycoBank MB827509).

Additional specimens examined. China, Fujian Prov., Sanming City, Sanming Nature Reserve of *Castanopsis kawakamii*, 260 m alt., 26 Aug. 2007, *Y.C. Li* 1022, HKAS 53367, *tef1α* sequence GenBank KF112304; Hunan Prov., Yizhang County, Mangshan, 4 Sept. 2007, 880 m alt., *Y.C. Li* 1087, HKAS 53432, *tef1α* and LSU sequences GenBank MH746438 and MH745969; Hainan Prov. Wuzhishan City, Wuzhushan National Nature Reserve, 2 Aug. 2009, 950 m, *N.K. Zeng* 416, FHMU 202, *tef1α* sequence GenBank MH746439.

Notes — The genus *Fistulinella* was originally described based on a species from Cameroon (Hennings 1901). It is characterised by the whitish to pink tubular hymenophore, the pinkish to brownish pink spore print, the smooth, elongate to fusiform, more or less dextrinoid basidiospores, and the presence of gelatinised structures in the pilei- and stipitipellis (Wu et al. 2014). *Fistulinella olivaceoalba* fits these characteristics rather well. It is recognised by the small slimy basidiomata with distinct greenish or olivaceous colours in the pileus and pinkish hymenophore. Microscopically long cylindrical septate cheilo- and caulocystidia, as well as fusiform pleurocystidia are also characteristic. Based on these features it is close to *F. cinereoalba* (Fulgenzi et al. 2010), which, however, lacks greenish colours in basidiomata and grows in South America. In GenBank this species is represented by the ITS sequence, which is significantly different from that of *F. olivaceoalba*.

There are no sequences of the type species, *Fistulinella staudtii*, available. But according to a 3-gene (*tef1α*, *rpb2*, LSU) phylogeny (Wu et al. 2014), a specimen from China (HKAS 53367) is grouping together with *Fistulinella prunicolor*, and belongs to the subfamily *Austroboletoideae*. However, they are rather distant – p-distance = 12.6 % difference of *tef1α* sequences. The genus *Fistulinella* appears to be polyphyletic and needs additional examination.

A BLASTn search of the ITS sequence of LE312004 in GenBank shows 99–100 % similarity with sequences obtained in the course of environment studies in Japan (e.g., GenBank LC315825 – ectomycorrhiza of *Pinus amamiana*, GenBank AB807905 – ectomycorrhiza of *Quercus*, and also GenBank AB973727 and AB509575).

Colour illustrations. Vietnam, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba National Park, Hon Giao Mt, upper montane mossy evergreen broadleaf forest, type locality; spores, SEM photos of spores, cheilocystidia, elements of pileipellis, caulocystidia, basidiomata in situ. Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

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Geastrum piquiriunense

Fungal Planet 842 – 14 December 2018

Geastrum piquiriunense Accioly, A.A. Lima, J.O. Sousa, M.P. Martín & Baseia, *sp. nov.*

Etymology. Name refers to 'Piquiri-Una' environmental preservation area in Rio Grande do Norte State, Brazil, where the type specimen was collected, around a community at the margins of Catu River. In Tupi-Guarani indigenous language, *piquiri* means 'river with little fishes'; *una* means black, dark.

Classification — *Geastraceae*, *Geastrales*, *Agaricomycetes*.

Immature basidiomata epigeous, orange-yellow ($N_{10}Y_{80}M_{30}$; Küppers 2002), subglobose, 3 mm high × 3 mm wide, rounded apex, surface not encrusted, hirsute, short hairs (< 0.5 mm high), presence of subicular base with rhizomorphs (up to 15 mm long), encrusted with debris. *Expanded basidiomata* saccate, 3.5–6 mm high (including peristome) × 10–18 mm wide. *Rhizomorphs* composed of up to 1 µm wide hyaline hyphae, covered by bipyramidal prism crystals (3.7–6.3 × 1.3–1.5 µm), not grouped to grouped, or in rose-shaped aggregates 3.8–11.4 × 3.6–11.4 µm. *Exoperidium* splitting into 5–6 revolute, and non-hygroscopic rays. *Mycelial layer* orange yellow ($N_{10}Y_{80}M_{40}$), persistent, surface not encrusted, hirsute, composed by small mycelial tufts (0.3–0.4 mm), densely organized, orange yellow ($N_{10}Y_{80}M_{40}$), formed by yellowish hyphae in 5 % KOH, not branched, 1.8–3.7 µm wide, lumen evident, with sinuous and thin walls (< 1 µm thick), surface not encrusted. *Fibrous layer* white to yellowish ($N_{00}Y_{00}M_{00}$ to $N_{00}Y_{10}M_{00}$), papery, composed of hyaline hyphae, 1.5–2.8 µm wide, with sinuous and thin walls (< 1 µm), not encrusted, lumen non-evident. *Pseudoparenchymatous layer* greyish brown ($N_{40}Y_{50}M_{40}$), persistent, formed by hyaline, subglobose, oval to elongated sphaerocysts, 21.3–60.8 µm high × 15.8–29.7 µm wide, thin-walled (< 1 µm thick). *Endoperidium* greyish brown ($N_{60}Y_{60}M_{40}$), globose to subglobose, 2–5 mm high (including peristome) × 3–7 mm wide, sessile, glabrous. *Peristome* finely fibrillose, delimited by a yellowish pale brown ($N_{10}Y_{20}M_{10}$) annulum, lighter than endoperidium, mammiform (< 1 mm high), 1.9–2.3 mm wide. *Gleba* powdery, darkened grey ($N_{99}Y_{00}M_{00}$). *Eucapillitium* brownish, 2.9–5.6 µm wide, not branched, surface encrusted, verrucose, lumen non-evident, tapering towards the end, thin walls (< 1 µm thick). *Basidiospores* subglobose, 4.7–6.3 µm diam (av. = 5.5 ± 0.4 × 5.3 ± 0.4 µm, Q_m = 1.03, n = 30), brownish in 5 % KOH, slightly flattened, conspicuous ornamentation at light microscopy, composed of confluent warts (0.2–0.5 µm high) with truncate apex, and irregularly distributed under SEM.

Habitat, Habit & Distribution — Specimens exhibited solitary to gregarious habit, on soil covered by leaf litter, in a clearing area. The type location presents Ombrophilous Dense Forest phytophysiognomy.

Colour illustrations. Brazil, Rio Grande do Norte, Área de Preservação Ambiental Piquiri-Una, where the specimens were collected; mature basidioma *in situ*, mycelial layer, capillitium under SEM, basidiospores under. Scale bars = 5 mm (basidioma), 1 mm (mycelial layer), 2 µm (capillitium and basidiospores). All photos from UFRN–Fungos 2892.

Typus. Brazil, Rio Grande do Norte, Goianinha, Área de Preservação Ambiental Piquiri-Una, Catú trail, alt. 64 m, S06°21'22.52" W35°12'57.86", on soil covered by leaf litter, 6 June 2016, *A.A. Lima & D.O. Andrade* (holotype UFRN-Fungos 2892, ITS and LSU sequences GenBank MH260269 and MH260270, MycoBank MB825194).

Additional species examined. ***Geastrum pusillipilosum***, Brazil, Paraíba, Mamanguape, REBIO Guaribas, SEMA II, 26 June 2014, *J.O. Sousa* JM100 (holotype UFRN-Fungos 2315, ITS and LSU sequences GenBank KX761175 and KX761176).

Notes — *Geastrum piquiriunense* is mainly characterised by its small basidiomata (up to 18 mm wide), hirsute mycelial layer, presence of a subicular base with rhizomorphs, delimited peristome, and subglobose basidiospores 4.7–6.3 µm, slightly flattened, with irregular confluent warts with truncate apex. This species is morphologically similar to *G. pusillipilosum* regarding its small size, hirsute mycelial layer, and delimited fibrillose peristome. *Geastrum pusillipilosum* can be recognised by its slightly larger, globose basidiospores (5–6.8 µm, Q_m = 1.0), covered by longer columnar warts (0.6–2 µm high; Crous et al. 2016a), and also by rhizomorphs covered by irregular oblique prism crystals, 2.5–2.8 × 4.8–8.6 µm. *Geastrum schweinitzii* and *G. pleosporum* also have small size basidiomata (up to 20 mm wide) and delimited peristome; however, G. *schweinitzii* has well-developed subiculum, caespitose growth, and smaller basidiospores (up to 5 µm diam) (Sousa et al. 2014), while *G. pleosporum* is characterised by smooth to subsmooth irregular shaped basidiospores up to 5 µm diam (Douanla-Meli et al. 2005). *Geastrum piquiriunense* could be also confused with *G. hirsutum*, but the latter can be distinguished by having longer and strigose mycelial tufts (up to 3 mm long) at its mycelial layer, and quite smaller basidiospores (2.5–3 µm wide) (Baseia & Calonge 2006, Silva et al. 2015). In our phylogenetic analysis *G. piquiriunense* grouped tightly with GenBank JN845120 (TENN:061141, MLbs = 99 %, PP = 1, MPbs = 100 %); nonetheless, this sequence is identified as *G. saccatum* both at the online database of University of Tennessee (TENN Herbarium) and the GenBank database, while in Kasuya et al. (2012), the same code (JN845120–TENN:061141) is identified as *G. sessile* (= *G. fimbriatum*, according to Index Fungorum). The hirsute mycelial layer clearly distinguishes *G. piquiriunense* from *G. saccatum* or *G. sessile* (= *fimbriatum*); moreover, these two species have predominantly smooth, sometimes felted or wrinkled mycelial layers (Sunhede 1989). In addition, *G. sessile* has an endoperidium with protruding hyphae and smaller basidiospores (2.7–5.2 µm diam) (Leite & Baseia 2007, Alfredo et al. 2016); also *G. saccatum* has smaller basidiospores (3.6–4.5 µm diam) (Leite et al. 2011). Thus, our analysis confirms a misidentification of collection TENN:061141, since it is not included in the clades of the sections *Corollina* nor *Fimbriata*; this collection needs to be morphologically reassessed in order to determine if it belongs to *G. piquiriunense*, or even if it is a new species awaiting description.

For supplementary information see MycoBank

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Ganoderma chocoense

Fungal Planet 843 – 14 December 2018

Ganoderma chocoense J.A. Flores, C.W. Barnes, & Ordoñez, *sp. nov.*

Etymology. Name refers to the locality were the species was collected.

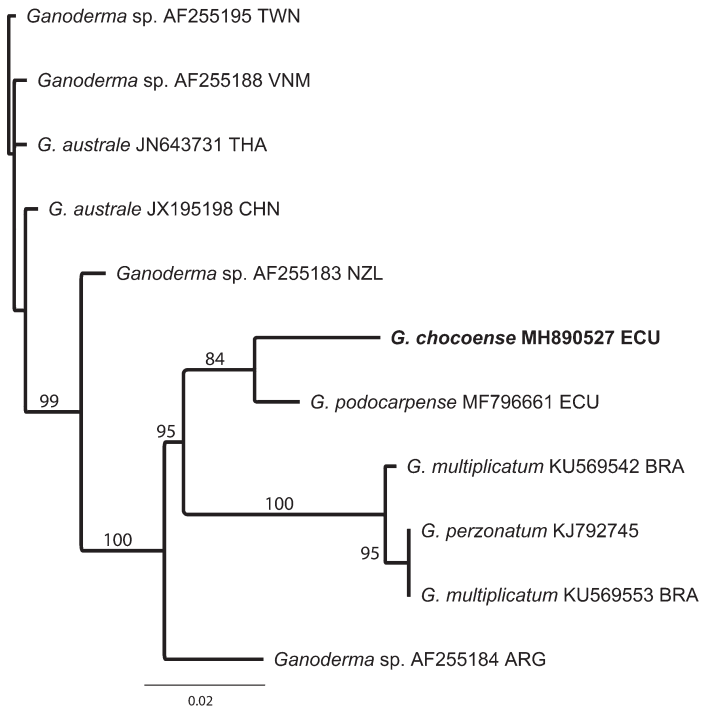
Classification — *Polyporaceae*, *Polyporales*, *Agaricomycetes.*

Basidiomata perennial, flattened, 5.5 × 3.8 cm, dimidiate with thicker base, woody, hard consistency when dry, pileus glabrous, sulcate, opaque, dark brown, covered with cinnamon coloured basidiospores, distinct cuticle in section of uniform width throughout the basidiomata, margin of light cream colour, context woody, 1.4 cm in width, no resin bands. *Hymenial surface* creamy white when fresh, ochre as it dries, turns darker upon contact, pores round, 6 per mm, thick wall, tubes dark brown, 0.4 cm wide, slightly stratified with white mycelium in the interior of old tubes. *Cutis* trichoderm. *Hyphal system* trimitic, generative hyphae yellowish, 1.5–3 µm wide, thin-walled, clamp connections present, skeletal hyphae brown, abundant, thick-walled to solid, up to 7 µm wide, connective hyphae very thin, hyaline, branched, 1.2 µm wide. *Basidia* not observed. *Basidiospores* double-walled, truncate, yellowish 8.9–11 × 4.7–6.4 µm, Q = 1.7.

Habit & Habitat — Solitary, on decomposing tree trunk.

Typus. Ecuador, Esmeraldas province, Chocó Tropical Rainforest, alt. 357 m, July 2012, *A. Salazar* (holotype QCAM 3123, Fungarium QCAM, ITS-LSU sequence GenBank MH890527, MycoBank MB827824, TreeBASE Submission ID 23292).

Notes — Morphologically, the sample belongs to the *G. applanatum* complex (Gottlieb & Wright 1999). The Neotropical Polypores key (Ryvarden 2004) indicates *G. australe* as the closest species. However, there are some morphological discrepancies, such as the shape and uniform thickness of the cuticle across the basidiocarp, the thickness of the tubes, the homogeneous context, lack of resin deposits, and the trimitic hyphal system in *G. chocoense*. Phylogenetically, *G. chocoense* is distinct from all taxa presently known to occur in the genus, with the closest species from the megablast search using the full ITS sequence being *G. podocarpense* (GenBank MF796661; 100 % Query Coverage, Identities = 544/568 (96 %), 11 gaps (1 %)). *Ganoderma podocarpense* was first described as a new species from Ecuador in 2017 (Crous et al. 2017b). Subsequent megablast hits are of *Ganoderma* species from Argentina and Brazil. The ITS phylogenetic tree of the top 10 megablast hits for the *G. chocoense* holotype sequence substantiates that it is a new species.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest 2.1.10 (Guindon & Gascuel 2003, Darriba et al. 2012) according to the Corrected Akaike Information Criterion (AICc). *Ganoderma* sp. (GenBank AF255195) represents the outgroup. Bootstrap support values > 80 % are given above branches. The phylogenetic position of *G. chocoense* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code, in order of appearance, is used, namely TWN: Taiwan, VNM: Vietnam, THA: Thailand, CHN: China, NZL: New Zealand, ECU: Ecuador, BRA: Brazil, and ARG: Argentina.

Colour illustrations. Ecuador, Chocó Tropical Rainforest; basidiocarps, basidiospores and skeletal hyphae. Scale bars = 10 µm.

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Geosmithia carolliae

Fungal Planet 844 – 14 December 2018

Geosmithia carolliae A.O.B. Cunha, A.R. Machado & Souza-Motta, *sp. nov.*

Etymology. The name refers to the host from which it was isolated, *Carollia perspicillata*.

Classification — *Incertae sedis*, *Hypocreales*, *Sordariomycetes*.

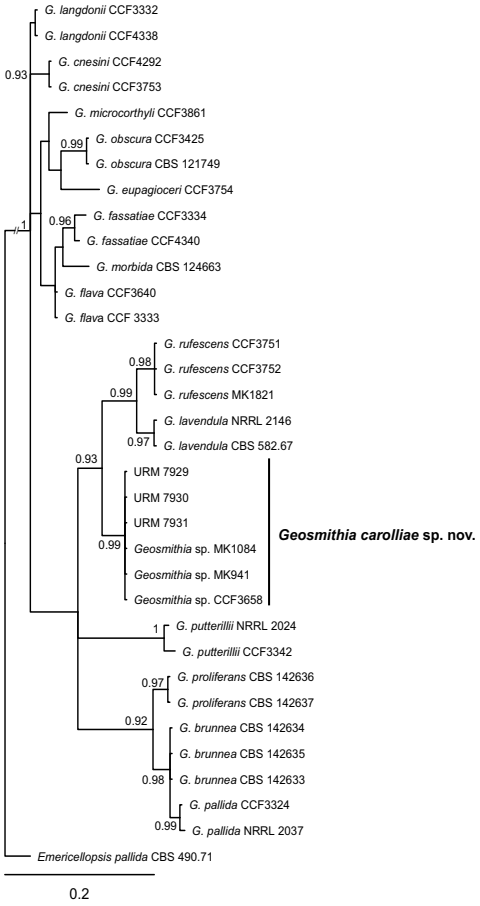
On MEA, 25 °C, 7 d: *Hyphae* hyaline, smooth, septate, 2–7.5 µm wide. *Conidiophores* hyaline, tall, septate, erect, solitary, often branched, mono- to quaterverticillate, verrucose, borne on hyphae, (23.5–)65–80(–104) × 1–1.5 µm. *Stipe* verrucose, (10.5–)26–49.5(–65) × 1–1.5 µm; branch (rami) verrucose, (10.5–)13–20.5(–26) × 1–1.5 µm. *Metulae* verrucose, (9.5–)10.5–11.5(–12.5) × 2–2.5 µm. *Phialides* verrucose, cylindrical to ellipsoidal, (4–)6.5–8.5 × 1.5–2 µm. *Conidia* hyaline, cylindrical to ellipsoid, smooth-walled, rounded at both ends, 4–5.5 × 2–2.5 µm; conidial chains up to 53 µm long, not persistent.

Culture characteristics — Colonies at 25 °C for 7 d. On MEA, the colonies are plane, dense, velutinous, opaque, ranging from rose vinaceous to rose greyish; reverse umber to pale brown; irregular margins, narrow and diffuse, ranging from salmon to white colours; pigmentation and exudate are absent, growing up to 50 mm. On CYA, the colonies are similar to MEA, but are pale vinaceous and the reverse vinaceous brown to dark brown, growing fast up to 70 mm. On CDA, the colonies are irregular, centrally filamentous, yeast-like aspect at the borders, umber to dark brown and margins salmon to white; reverse pale brown to yellowish; slight yellowish pigmentation around the colony, exudate absent, growing up to 20 mm. Colonies at 37 °C for 7 d. On MEA and CYA are similar, planes, dense, velutinous to floccose, opaque, ranging from pale brown to greyish, reverse umber to dark brown; margins, narrow and diffuse, ranging from pale vinaceous to buff, pale brown to pale yellow; pigment and exudate absent, growing up to 0.5 mm. On CDA, the colonies are similar to CDA at 25 °C, but are white to pale cream and the reverse umber to dark brown, growing up to 0.6 mm.

Typus. Brazil, Pernambuco state, Tupanatinga, Catimbau National Park, Bat cave 'Meu Rei', S08°29'14.1" W37°16'48.8", isolated from the bat wing of *Carollia perspicillata*, 20 Sept. 2017, *A.O.B. Cunha & E. Barbier* (holotype URM 91977, culture ex-type URM 7929, ITS, LSU and *tub2* sequences GenBank MH989506, MH989510 and MH989534, MycoBank MB827978).

Additional material examined. Brazil, Pernambuco state, Tupanatinga, Catimbau National Park, Bat cave 'Meu Rei', S08°29'14.1" W37°16'48.8", isolated from the bat wing of *Carollia perspicillata*, 20 Sept. 2017, *A.O.B. Cunha & E. Barbier*, URM 7930 and URM 7931. URM 7930: ITS, LSU and *tub2* sequences GenBank MH989507, MH989511 and MH989535; URM 7931: ITS, LSU and *tub2* sequences GenBank MH989508, MH989512 and MH989536.

Notes — The genus *Geosmithia* was proposed by Pitt (1979) to accommodate *Penicillium lavendulum* and related species. Since its description, 20 species were included in it according to Index Fungorum and MycoBank databases (25 Sept. 2018). BLASTn searches using ITS sequences of *G. carolliae* demonstrated that they are identical to sequences deposited as *Geosmithia* sp. living in association with bark beetles in the Mediterranean area (Kolařík et al. 2007). These sequences grouped together with our sequences in the phylogenetic tree, and here they are named as *G. carolliae*. The LSU sequences have high identities (99 %) to sequences from *G. lavendula* (e.g., GenBank MH867927.1, Vu et al. 2019), amongst other. The *tub2* sequences have *G. morbida* (GenBank KF853911.1) as the closest identity (89 %). *Geosmithia carolliae* is phylogenetic related and morphologically similar to *G. lavendula*, but differ from it by culture characteristics (growth on MEA and CYA at 25 °C up to 35 mm and on CYA at 37 °C up to 12 mm), and by the size and ramification of conidiophores (200–400 × 3–3.5 µm), rami (15–25 × 3–3.5 µm), metulae (12–15 × 3–3.5 µm), phialides (10–12 × 2.2–2.5 µm) and conidia (4–5.5 × 2–2.5 µm) (Pitt 1979). Also, *G. carolliae* differs from *G. rufescens* by culture characteristics (growth on MEA at 25 °C up to 30 mm and on CYA up to 22 mm; no growth at 37 °C), and by the size and ramification of conidiophores (30–70 µm), rami (15–30 µm × 2–3 µm), metulae (9–11 × 2–2 µm), phialides (8.5–11.5 × 2–2.5 µm) and conidia (3–5 × 1.5–2.5 µm) (Kolařík & Kirkendall 2010).



Bayesian inference tree obtained by analysis of ITS rDNA sequences in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The nucleotide substitution model used was GTR+I+G. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold** face. *Emericellopsis pallida* (CBS 490.71) was used as outgroup.

Colour illustrations. *Carollia perspicillata* during collection in the Catimbau National Park; colony on MEA after 7 d at 25 °C, conidiophores and conidia. Scale bars = 10 µm.

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Geosmithia xerotolerans

Fungal Planet 845 – 14 December 2018

Geosmithia xerotolerans Rodr.-Andrade, Cano & Stchigel, *sp. nov.*

Etymology. From Greek *ξερός*-, dry, and Latin *-tolerans*, tolerance, due to the ability of this fungus to grow on culture media with a low water activity.

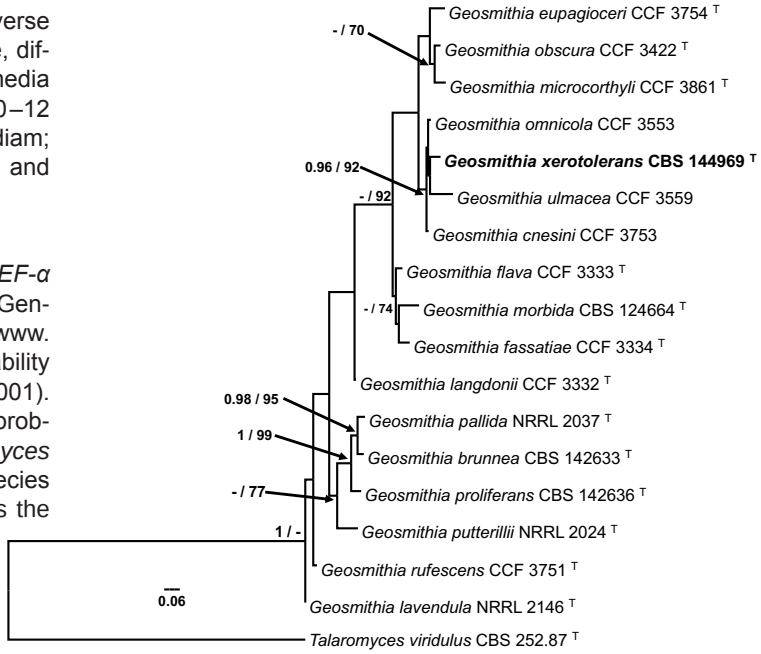
Classification — *Incertae sedis*, *Hypocreales*, *Sordariomycetes.*

Mycelium composed of hyaline, septate, funiculose hyphae, 2–3 µm wide. *Conidiophores* borne on vegetative mycelium, determinate, erect, septate, penicillate, bi- to terverticillate, mostly solitary, sometimes funiculose; stipes hyaline, 25–155 × 2–3 µm, septate, smooth-walled to verrucose, asymmetrically branched; primary branch (= rami) cylindrical, 20–40 × 2–3 µm, mostly septate, smooth-walled to verrucose; terminal branch (= metulae) cylindrical, 7–15 × 2 µm, rarely 1-septate, with smooth to verrucose walls, in whorls of 2–3; phialides cylindrical, 8–10 × 1.5–2 µm, abruptly tapering at the apex, with smooth to verrucose walls, in whorls of 2–5. *Conidia* hyaline, aseptate, ellipsoid to ovoid, 3–4 × 1.5–2 µm, rounded at both ends, smooth-walled, disposed in chains of up to 20 conidia. *Sexual morph* not observed.

Culture characteristics — *Colonies* on MEA reaching 38–39 mm diam after 2 wk at 25 °C, slightly elevated, powdery, margins irregular, orange white (5A2; Kornerup & Wanscher 1978) at centre and white (5A1) at edge, exudates absent, sporulation abundant; reverse orange (6A6), diffusible pigment absent. Colonies on CYA reaching 49–51 mm diam after 2 wk at 25 °C, slightly elevated, powdery, margins regular, white (4A1) at centre and pale yellow (4A3) at edge, exudates absent, sporulation abundant; reverse reddish orange (7B7) at centre and pale orange (6A5) at edge, diffusible pigment absent. Colonies on CZD 62–63 mm diam after 2 wk at 25 °C, cottony, margins irregular, white (3A1), exudates absent, sporulation abundant; reverse yellowish white (3A2), diffusible pigment absent. Colonies on YES reaching 62–63 mm diam after 2 wk at 25 °C, slightly elevated with radial waves, reddish grey (12B2) and white (4A1), exudates absent, sporulation abundant; reverse reddish brown (9E7) at centre and orange (6A6) at edge, diffusible pigment absent. This fungus grows on culture media with a low water activity (on DG18 after 2 wk at 25 °C, 10–12 mm diam; on G25N in the same conditions, 27–29 mm diam; on MY70S, 39–40 mm diam; and on MEA with 30, 40 and 50 % (glucose 50 % / fructose 50 %), 23–24 mm diam, 18–19 mm diam and 12–13 mm diam, respectively). In these culture media the fungal sporulation is abundant. Minimum, optimal and maximum temperature of growth: 15 °C, 25 °C and 35 °C, respectively.

Typus. Spain, Tarragona province, Els Pallaresos, isolated from a darkened wall of a house, 19 Apr. 2018, *J. Cano & A.M. Stchigel* (holotype CBS H-23734, cultures ex-type FMR 17085 = CBS 144969; *BenA*, *EF1-α*, ITS and LSU sequences GenBank LS998791, LS998792, LS998789 and LS998790; MycoBank MB827825).

Notes — *Geosmithia xerotolerans* was recovered from the surface of a darkened house wall taken in Els Pallaresos, Tarragona province, Spain. The genus *Geosmithia* was erected to accommodate species previously placed in *Penicillium*, with the following differentiable combination of characters: colonies in colours other than greyish blue or greyish green, penicillate and roughened conidiophores, with both phialides and conidia cylindrical (Pitt 1979). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is the ex-type strain of *Geosmithia cnesini* MK 1820 (GenBank AM947671; Identities = 965/978 (99 %), 1 gap (0 %)); using the LSU sequence it was *Geosmithia microcorthyli* CCF3861 (GenBank MG954241; Identities = 809/815 (99 %), no gaps); using the *EF1-α* sequence, it was *Geosmithia omnicola* CNR8 (GenBank KR135476; Identities = 238/280 (85 %), 13 gaps (4 %)); and using the *BenA* sequence it matched with *Geosmithia omnicola* CNR43 (GenBank KP990575; Identities = 429/460 (93 %), 9 gaps (1 %)). Our ITS-*BenA*-*EF-α* phylogenetic tree corroborated the placement of our isolate as a new species of *Geosmithia*, being phylogenetically close to *Geosmithia omnicola.*



Maximum likelihood tree obtained from the ITS-*BenA*-*EF-α* alignment of our isolate and sequences retrieved from GenBank. The tree was built by using RAxML CIPRES (http://www.phylo.org/sub_sections/portal/) and the analysis of probability was run in MrBayes v. 3.2.1 (Huelsenbeck & Ronquist 2001). Bootstrap support values ≥ 70 % and Bayesian posterior probability values ≥ 0.95 are presented at the nodes. *Talaromyces viridulus* CBS 252.87 was used as outgroup. The new species proposed in this study is indicated in **bold**. T represents the ex-type strain of the novel species.

Colour illustrations. Darkened wall in Els Pallaresos, Tarragona province, Spain; colonies growing on different culture media (MEA, CYA, CZD and YES at 25 ºC) and conidiophores. Scale bars = 10 µm.

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Henningsia resupinata

Fungal Planet 846 – 14 December 2018

Henningsia resupinata A.M.S. Soares & Ryvarden, *sp. nov.*

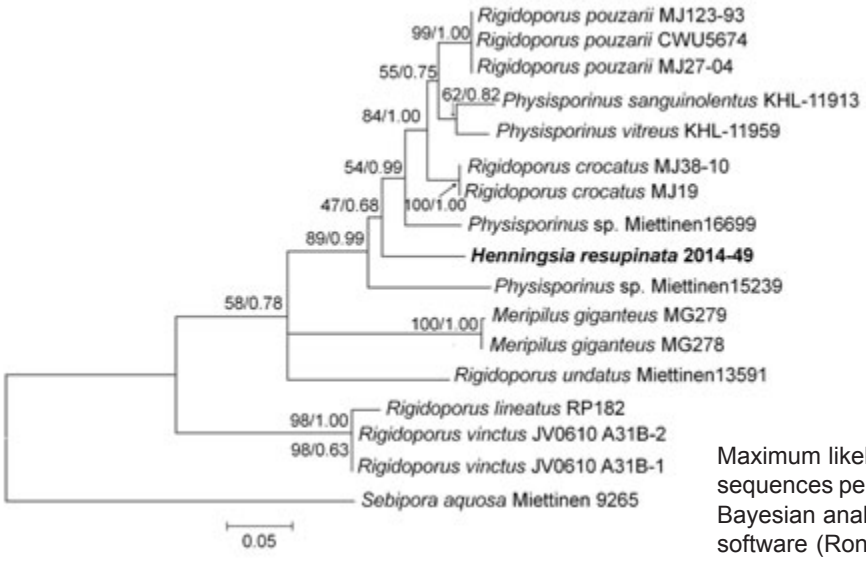
Etymology. (L.) *resupinata*, bent, referring to the shape of the basidiomata.

Classification — *Meripilaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, resupinate, 2–4 cm wide and long and 1 mm thick, adnate, fleshy and white when fresh (2B) becoming distinct rusty red when bruised after collecting, hard and fragile and black when dry (black 37) (Watling 1969), pores irregular, about 1–2 mm in the sloping substrate, in other parts of the holotype more regular and 4–5 pores per mm, tubes concolorous with the pore surface. Context almost absent, dense and black when dry (37). *Hyphal system* monomitic; generative hyphae with simple septa, hyaline to pale yellow, thin-walled, 3–6 µm wide. *Gloeoplerous hyphae* and *cystidia* absent. *Basidia* not seen. *Basidiospores* 4–5 µm diam, globose to subglobose, smooth, thin-walled, IKI-.

Typus. Brazil, Amapá, Porto Grande, Serra da Capivara, on dead wood, 2014, *A. Soares* 2014-49 (holotype URM, isotype O, ITS and LSU sequences GenBank MG255826, MycoBank MB823555).

Notes — The black basidiomata when dry, the simple septate hyphae and the globose to subglobose basidiospores clearly place this species in *Henningsia* where all species share the same colour and simple septate generative hyphae. *Henningsia resupinata* can be separated from the other species of the genus by the resupinate basidiomata. *Henningsia macrospora* is another species also found in Brazil and also has a black basidioma when dry, but it is separated by the pileate basidiomata with numerous gloeoplerous hyphae in the context and the larger, subglobose to ellipsoid basidiospores (6–7 × 4.5–5 µm) (Gibertoni & Ryvarden 2014). In the phylogenetic tree, *H. resupinata* clustered with low support with *Physisporinus* sp. (47 %/0.68) collected in Indonesia and it is distantly related to *P. sanguinolentus* (KHL_11913) collected in Norway. *Physisporinus sanguinolentus* is similar by the white basidiomata when fresh and becoming bright rusty red when bruised or greyish to blackish on drying. However, the pores in *P. sanguinolentus* are smaller (8–10 per mm) and the basidiospores are larger and ovoid to subglobose (6–7 × 5–6 µm). Besides, *P. sanguinolentus* has fusoid cystidioles (15–27 × 5–6 µm) which are lacking in the new species (Ryvarden & Gilbertson 1994). There is no molecular data regarding *Henningsia*, and, for the time being, the new species will be kept in this genus due its morphological characters. Moreover, *Henningsia* is a Neotropical genus and the type species is from Brazil, while *Physisporinus* occurs mostly in Europe.



Maximum likelihood phylogenetic tree inferred from ITS+LSU sequences performed with RAxML v. 7.0.4 (Stamatakis 2006). Bayesian analysis (BY) was performed with MrBayes v. 3.2.1 software (Ronquist et al. 2012) for 5 M generations with four Markov chains, and trees sampled every 1 000 generations, similar topology was obtained (not shown). Bootstrap support values (1 000 replicates) and posterior probabilities (PP) from Bayesian analysis to each node are shown from left to right. The new species described in this study is in **bold** face. *Sebipora aquosa* represents the outgroup. The alignment is deposited in TreeBASE (ID 22819).

Colour illustrations. Environment where the type specimen was collected in Porto Grande, Serra da Capivara, Amapá, Brazil; *Henningsia resupinata* fresh basidiomata (top), dried basidioma, generative hyphae and basidiospores (bottom). Scale bars = 2 cm (basidiomata), 20 µm (generative hyphae), 10 µm (basidiospores).

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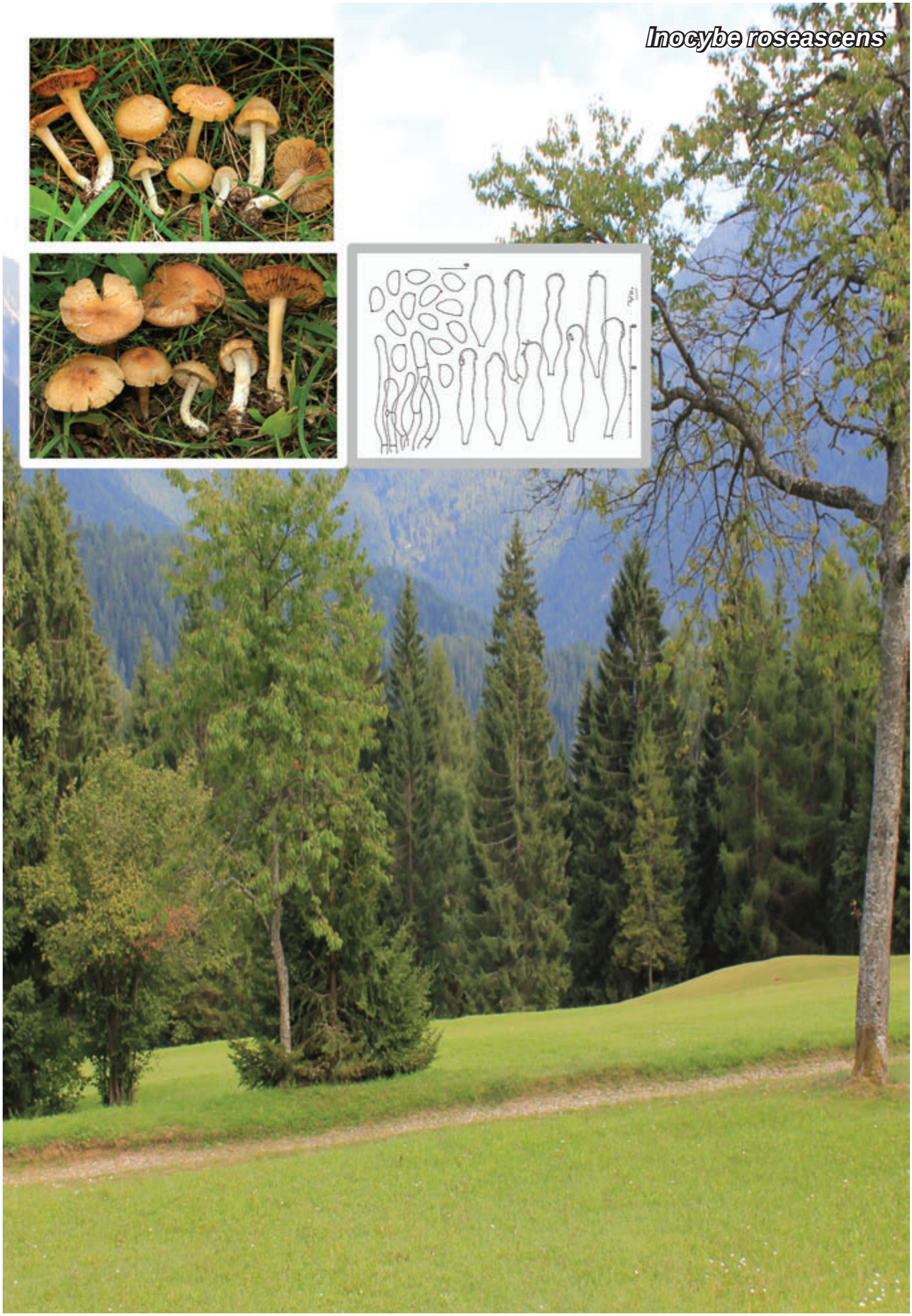

Inocybe roseascens

Fungal Planet 847 – 14 December 2018

Inocybe roseascens Bizio, Bahram, Tedersoo, Orzes & Saitta, *sp. nov.*

Etymology. Refers to the colour of the pileus and stipe.

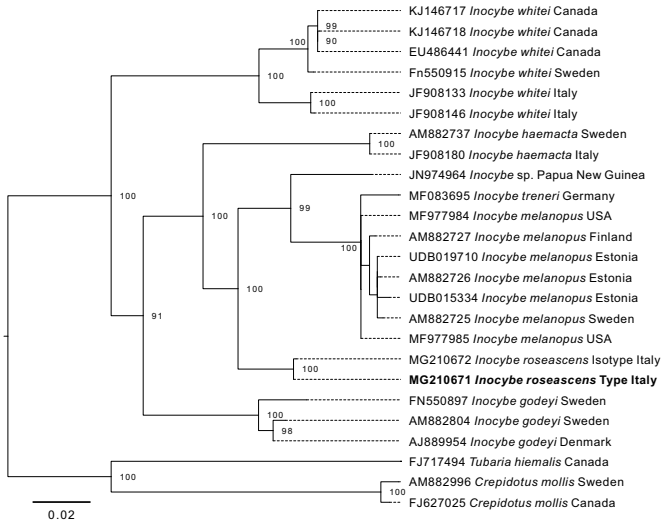
Classification — *Inocybaceae, Agaricales, Agaricomycetes.*

Pileus up to 40 mm, widely campanulate, then convex to plane, with central umbo, obtuse and irregular profile, with sulcated-cracked margin. *Cuticle* fibrillose-rimose, slightly chapped-squamulose, more cracked at the centre; colour yellowish to bread crust (Munsell 7.5YR: 8/6, 7/8; 10YR: 7/8; 2.5Y: 7/8), then pinkish, old-pink to orange-fulvous and reddish bronze all over the basidioma (Munsell 2.5YR: 6/8; 5YR: 7/8; 7.5YR: 7/8; 10YR: 7/8). *Cortina* white, observed in early stages. *Lamellae* close, thick, colour very light (Munsell 2.5Y: 8/3-4), then ochraceous, olivaceous (Munsell 2.5Y: 7/6) to rust-concolorous (Munsell 2.5Y: 7/8), white floccose edge, crenulated. *Stipe* 40–50 × 3–7 mm cylindrical, pruinose on the upper part, first whitish to straw coloured (Munsell 2.5Y: 8/3-4), then grey to grey-rose pale, concolorous with pileus; covered with coarse, long, and whitish fibrils. *Flesh* white, firm, red staining absent, *smell* absent. *Basidiospores* (7.5–)8.2–10(–10.7) × (5–)5.3–6.2(–6.6) µm, Q = (1.2–)1.3–1.5(–1.7), smooth, subamygdaliformis, with small soprapicular depression and variable apex, obtuse to subconic and rarely conic-papillate; germinative pore sometimes visible. *Basidia* 35–40 × 9–12 µm, tetrasporic. *Paracystidia* not observed. *Hymenial cystidia* 50–85 × 10–15 µm cylindrical or slightly clavate, clavate-subutriformis, sinuose, subcapitate to capitate, not lageniforme; wall 0.5–1(–2) µm thick, without oxalate crystals calcium or rarely present; NH_3-. *Caulocystidia* only in the upper part of the stipe, (1/4), 100 × 10 µm, flexuose, subcylindrical, catenulate.

Typus. Italy, Veneto, Agordo, loc. Campon, N46.30010 E12.05280, 1 300 m asl, mixed forest of *Picea abies* and *Corylus avellana*, 2015, *R. Orzes* (holotype MCVE29329, ITS-LSU sequence GenBank MG210671; ibid., 2015, *E. Bizio*, paratype TU124466, ITS-LSU sequence GenBank MG210672, MycoBank MB823058).

Notes — Only two *Inocybe* species with smooth spores, *I. whitei* and *I. godeyi*, have both metuloid cystidia and a reddening surface, as in the new species proposed here. The basidiomata of *I. roseascens* are at first yellow-ochre, which gradually turn reddish, but this is not the case in its odourless flesh. Based on a morpho-chromatic point of view, *I. roseascens* is close to the group of *I. withei*, because of its partially cystidiate stipe and the absence of basal bulb. *Inocybe godeyi* has ochre to orange-fulvous-red, brick-pink or rarely red carmine sporocarps, and it belongs to the supersection *Marginatae* because of its fully cystidiate stipe and marginate basal bulb. Our phylogenetic analysis showed that *I. godeyi* is closer to *I. roseascens* than *I. whitei*. The flesh of *I. godeyi* is white when cut and it quickly turns to orange-red, concolorous to the external surface (Alessio & Rebaudengo 1980). Because the flesh of *I. roseascens* does not change colour when damaged, and the absence of smell, it cannot be placed in the section *Lactiferae*, and it most likely belongs to the supersection *Cortinatae* (Boursier & Kühner 1928). Species in *Cortinatae* have a cortina at young states, and a stipe that is slightly pruinose at the apex only, or not at all.

Based on our molecular analysis, the closest species to *I. roseascens* is *I. melanopus*, a species described from Northern America and well known in Europe (Kuyper 1986, Stangl 1989, Bon 1997, Alpago Novello 2006, Bizio 2012). *Inocybe melanopus* was first described by Stuntz as *I. melanopoda* (Stuntz 1954), as cited in Index Fungorum. However, it is universally accepted with the orthographic variant *I. melanopus*. *Inocybe melanopus* is not a reddening species, with stipe dark brown to blackish, pileic surface lanose feltrate, ochraceous to beige with infrequent cystidia, cylindrical-fusiform, caulocystidia absent. In *I. roseascens*, the stipe is never blackish.



The data matrix was aligned in MAFFT v. 7 (Katoh & Standley 2013). A phylogeny was constructed under maximum likelihood (ML), and ML bootstrap support values (100 replicates) were obtained as implemented in RAxML Blackbox (http://embnet.vital-it.ch/raxml-bb/) with the default settings. The alignment and tree are deposited in TreeBASE (Submission ID 22854).

Colour illustrations. Campon, Agordo, Italy, mixed forest of *Picea abies* and *Corylus avellana*; *Inocybe roseascens*, basidiomata in habitat, basidiospores, hymenial cystidia caulocystidioid.

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Kwoniella endophytica

Fungal Planet 848 – 14 December 2018

Kwoniella endophytica A.M. Glushakova & Kachalkin, *sp. nov*

Etymology. Name refers to the original endophytic isolations from different fruit tissues.

Classification — *Cryptococcaceae*, *Tremellales*, *Tremellomycetes*.

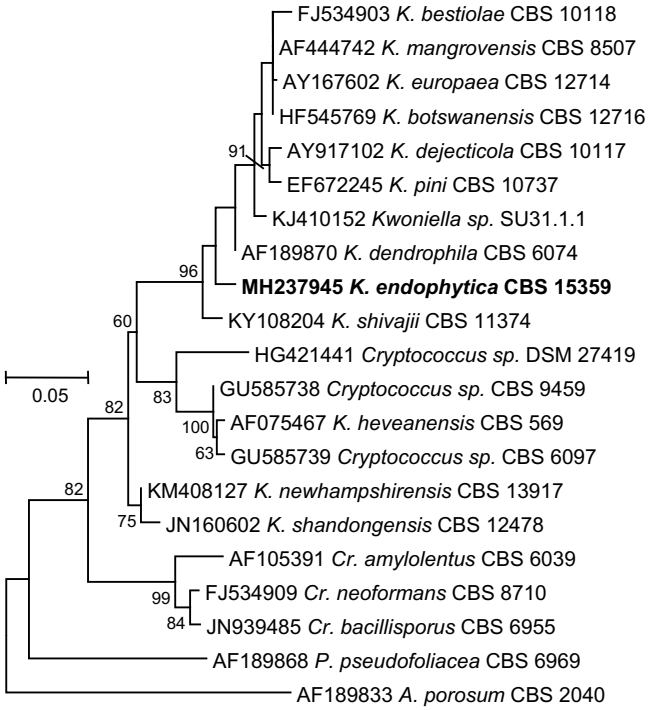
On potato dextrose agar (PDA) and 2 % glucose yeast nitrogen base agar (YNB), after 7 d at 22 °C, streak is white, butyrous, smooth surface and an entire straight margin. Cells are subglobose to globose, 5–6 × 4–5 µm, occur singly, in pairs and in clusters, divide by multilateral budding, cells with one or two buds. On glucose peptone yeast extract agar (GPYA), after 7 d at 22 °C, streak colonies are cream, cells are mostly globose, 5–7 × 5–6 µm, occur singly and in pairs, *divide by multilateral budding*, budding is single. Pseudohyphae, ballistoconidia and sexual structures have not been observed during 1–2 wk in culture (pure cultures and in mating test) grown on YNB agar, GPYA, PDA and cornmeal agar. Glucose is not fermented. Glucose, galactose, D-ribose, D-xylose, L-arabinose, D-arabinose, L-rhamnose, sucrose, maltose, trehalose, cellobiose, lactose, raffinose, melezitose, inulin (variable), soluble starch (variable), glycerol, ribitol, D-glucitol, D-mannitol, galactitol, *myo*-inositol, ethanol, 2-keto-D-gluconate, 5-keto-D-gluconate, D-gluconate, D-glucoronate, DL-lactic acid (weak) and succinic acid are assimilated; no growth occurs on L-sorbose, D-glucosamine, methyl alpha-D-glucoside, salicin, arbutin, melibiose, erythritol, methanol, citric acid, propane-1,2-diol, butane-2,3-diol and hexadecane. Nitrogen compounds: ammonium sulfate, potassium nitrate (variable), L-lysine are assimilated. Growth on vitamin-free medium, on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth is absent with 0.01 % cycloheximide, on YM agar with 10 % NaCl. Positive result for the Diazonium blue B reaction and for urease activity. Starch-like compounds are produced. Maximum growth temperature is 31–32 °C.

Typus. Russia, Moscow, Kuskovo from the hypanthium of pear fruit *(Pyrus communis)*, Aug. 2015, *A.M. Glushakova* (holotype OK21, ex-type cultures KBP Y-5323 = VKM Y-3035 = DSM 106749 = CBS 15359, SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MH237944, MH237945, LS992196 and LS992197, MycoBank MB825499).

Additional specimens examined. Russia, Moscow region, Lobnya, from the hypanthium of apple (*Malus communis*), Aug. 2015, *A.M. Glushakova*, KBP Y-5326; Moscow, Rublevo, from the hypanthium of pear fruit *(Pyrus communis)*, Aug. 2015 and Sept. 2015, *A.M. Glushakova*, KBP Y-5327 and KBP Y-5328; Moscow, Rublevo, from the hypanthium of cherry *(Cerasus* sp.), Sept. 2015, *A.M. Glushakova*, KBP Y-5329; Moscow, Kuskovo, from the hypanthium of pear fruit *(Pyrus communis)*, Sept. 2015, *A.M. Glushakova*, KBP Y-5330 and KBP Y-5331; Moscow, Karacharovo, from the hypanthium of apple (*Malus communis*), June 2015, *A.M. Glushakova*, KBP Y-5332, ITS sequences GenBank MH337639–MH337645.

Colour illustrations. Russia, Moscow, pear fruits on tree; growth of yeast colonies on YNB agar, morphology of cells on YNB agar and GPYA (after 7 d at 22 °C). Scale bars = 10 µm.

Notes — Analysis of the ITS region of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Kwoniella*. Based on NCBIs GenBank database, the best hit using the ITS sequence is *K. botswanensis* CBS 12716, GenBank NR_119822 (96 %, 10 subst. and 7 gaps), using LSU it is *K. dendrophila* CBS 6074, GenBank NG_058326 (98 %, 12 subst.), using SSU it is *K. mangrovensis* CBS 8507, GenBank KF036681 (99 %, 10 subst.), *K. shivajii* CBS 11374, GenBank KF036652 (99 %, 9 subst. and 1 gap), using *TEF1* it is *K. dendrophila* CBS 6074, GenBank FJ534856 (95 %, 15 subst.), and using *RPB1* it is *K. dendrophila* CBS 6074, GenBank KF036320 (82 %, 147 subst.). In compliance with a recent revision of the genus (Liu et al. 2015), the phylogenetic placement of the new species is demonstrated using the LSU rDNA phylogeny. No growth on L-sorbose, methyl alpha-D-glucoside, salicin, citric acid, methanol, YM agar with 10 % NaCl and growth on DL-lactic acid, 50 % w/w glucose / yeast extract (0.5 %) agar are good physiological tests for the distinction of the new species from the phylogenetically closely related species of the genus.



Maximum likelihood (ML) tree obtained from the analysis of LSU sequence data. Bootstrap support values above 55 % are shown at the nodes. The alignment included 455 bp and was performed with MAFFT v. 7. The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Phylogenetic analysis was conducted in MEGA v. 6.

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Lareunionomyces loeiensis

Fungal Planet 849 – 14 December 2018

Lareunionomyces loeiensis Pinruan, Nuankaew & P. Khamsuntorn, *sp. nov.*

Etymology. Refers to the location where the fungus was collected, Loei province, Thailand.

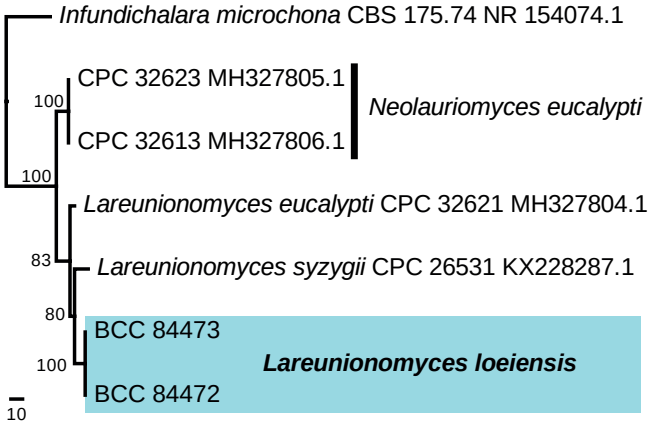
Classification — *Neolauriomycetaceae*, *Helotiales*, *Leotiomycetes.*

Conidiophores solitary, erect, dark brown, thick-walled, smooth, straight, subcylindrical, unbranched, 2–3-septate, 90–150(–165) × 5–6.5 µm, base lacking rhizoids. *Penicillate conidiogenous apparatus* brown to pale brown, smooth; primary branches brown, smooth, aseptate, subcylindrical to clavate, 6–8 × 3–6.5 µm, giving rise to 6–8 secondary branches; secondary branches pale brown, subcylindrical to clavate, 6–7.5 × 3–4 µm; tertiary branches pale brown, 4–5 × 2–3 µm, giving rise to several conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, 12–14 × 1.5–2 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base truncate, 4.5–5.5 × 1.5–2.5 µm, in long chains.

Culture characteristics — Colonies on PDA reaching up to 5 cm diam after 4 wk at 25 °C, with spreading, smooth surface; margins smooth, sparse aerial mycelium, surface pale brown to cream, reverse pale brown. Sporulation on PDA after incubation at 25 °C for 30 d.

Typus. Thailand, Loei, on leaves of unknown tree, 12 Feb. 2017, *P. Khamsuntorn* (holotype BBH 43483, culture ex-holotype BCC 84473 ITS and LSU sequences GenBank MK047459.1 and MK047509.1, culture ex-isotype BCC 84472, ITS and LSU sequences GenBank MK047460.1 and MK047510.1, MycoBank MB827980).

Notes — The genus *Lareunionomyces* was established by Crous et al. (2016b), with *L. syzygii* as the type species. *Lareunionomyces loeiensis* is designated as a new species based on both morphological characteristics and phylogenetic analyses. *Lareunionomyces loeiensis* is similar to *L. syzygii* and *L. eucalypti*, but distinct from them in that it has conidia aggregating in longer chains that form a mucoid spore mass. Conidiophores are longer than those of *L. syzygii* (50–100 × 5–8 µm) and similar to those of *L. eucalypti* (60–160 × 5–6 µm) but up to 3-septate only while other are 2–7-septate. Conidia of *L. loeiensis* are slightly wider than those species, the apex and base are truncate, and occur in long chains.



Single most parsimonious tree obtained from the ITS alignment using PAUP v. 4.0b10 (Swofford 2003; seven sequences including the outgroup, 518 included characters of which 28 were parsimony-informative). The tree was rooted with *Infundichalara microchona* (GenBank NR_154074.1). The novel species described here is indicated in ***bold italic*** text. The scale bar represents the number of changes and parsimony bootstrap support values > 50 % from 1 000 replicates are indicated at the nodes.

Colour illustrations. Leaf litter in Thailand (background photo); fungus growing on the substrate (scale bar = 100 µm), conidiophores (50 and 25 µm), conidiogenous head with phialides (10 µm), conidia (10 µm), colonies on PDA after 3 wk; (left) above (right) and below, conidiophores in culture from sporulating colony (50 µm).

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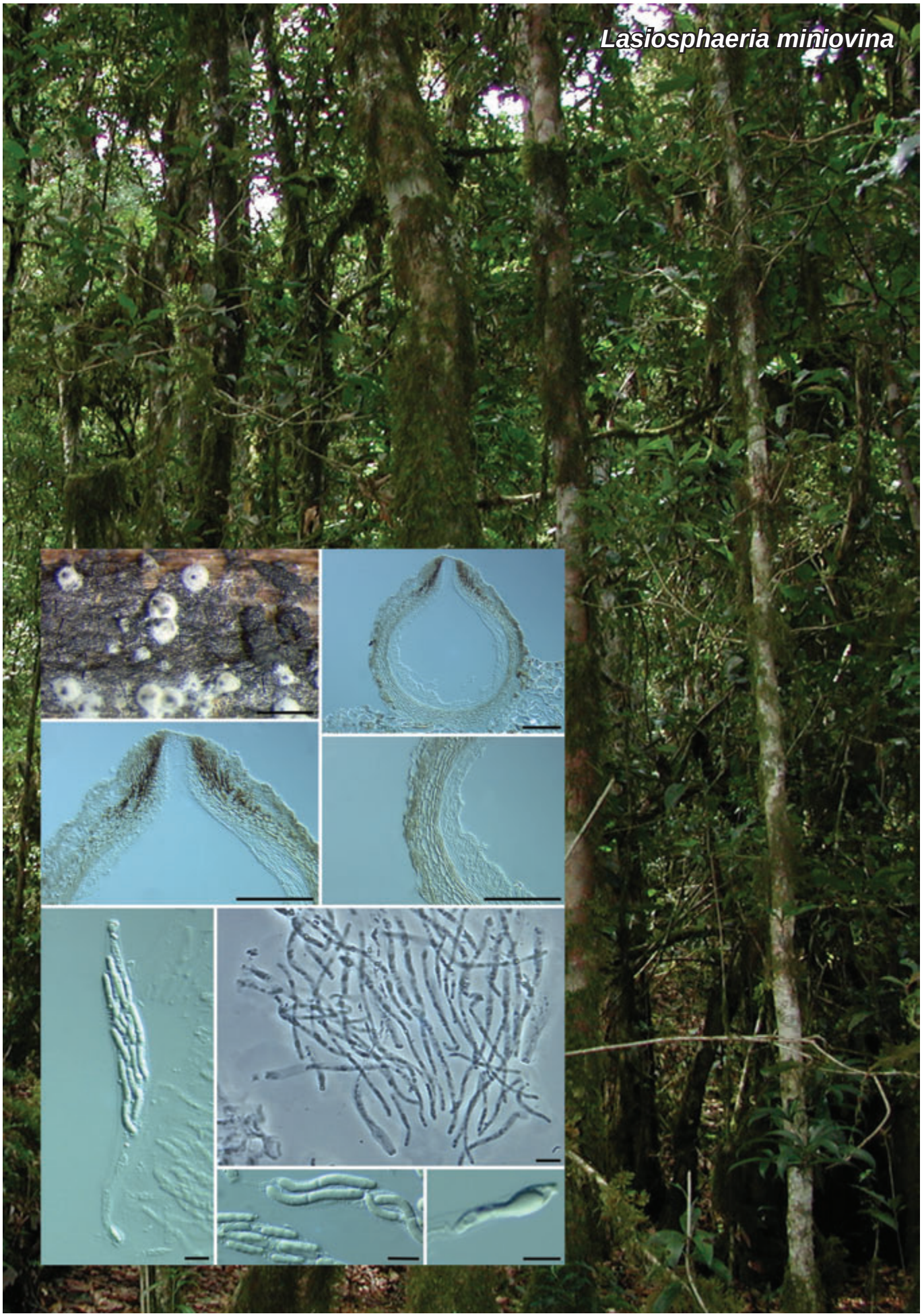

Lasiosphaeria miniovina

Fungal Planet 850 – 14 December 2018

Lasiosphaeria miniovina A.N. Mill. & Huhndorf, *sp. nov.*

Etymology. The specific epithet refers to this species resembling a smaller version of *L. ovina*.

Classification — *Lasiosphaeriaceae*, *Sordariales*, *Sordariomycetes*.

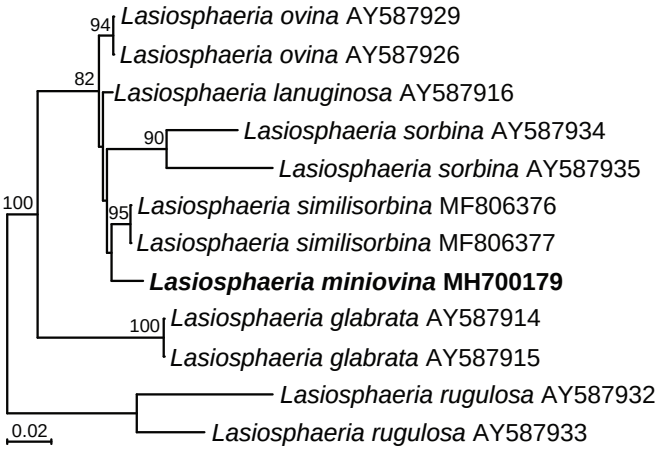
Ascomata ampulliform to ovoid, papillate, 200–250 µm diam, 200–350 µm high, numerous, scattered to gregarious, superficial; young ascomata tomentose, white, tomentum becoming tightly appressed, crust-like and cream to waxy and brownish grey with age, areolate, finally tomentum wearing away and ascomata becoming black and glabrous; neck conical, glabrous, black. *Ascomatal wall* of *textura angularis* in surface view, in longitudinal section 3-layered, 20–40 µm thick, inner layer pseudoparenchymatous, 5–8 µm thick, composed of 3–5 layers of elongate, flattened, pale brown cells, middle layer pseudoparenchymatous, 10–16 µm thick, composed of 3–5 layers of polygonal to angular, pale brown cells, outer layer prosenchymatous, 5–16 µm thick, composed of several to few layers of hyphae depending on age of ascomata, hyphae 1–2.5 µm wide, hyaline to pale brown, septate, thin-walled. *Ascomatal apex* with periphyses. *Centrum* with yellow pigments that quickly diffuse in water. *Paraphyses* filiform, 2–5 µm wide, longer than asci, hyaline, numerous, septate, unbranched, persistent. *Asci* cylindrical, 85–130 × 8–14 µm, stipitate, stipe 24–46 × 2.5–4.5 µm, numerous, unitunicate, thin-walled, apex truncate; ring narrow, shallow, refractive; subapical globule smooth, 2–4 µm wide; with 8 bi- to triseriate ascospores. *Ascospores* cylindrical, ends rounded, 22–33 × 2.5–4.5 µm (av. 28 ± 2.5 × 3.5 ± 0.5), straight when first produced, hyaline, aseptate, without appendages; becoming sigmoid to geniculate, 1-septate, after liberation from the ascus head slightly swelling up to 5.5 µm wide, remaining hyaline, rarely becoming up to 7-septate with age, hyaline to yellowish, occasionally producing phialides directly from the ascospores.

Habitat — Decayed wood in a tropical forest.

Distribution — Known only from Costa Rica.

Typus. Costa Rica, San Jose, San Gerardo de Dota, Albergue de Montage, Savergre, Sendero la Quebrada, on 10 cm branch with loose bark, N9.33 W83.48, 701 m elev., 12 May 1996, *S.M. Huhndorf & F.A. Fernandez* (holotype SMH 2392 (F), isotype at ILLS, ITS-LSU sequence GenBank MH700179, MycoBank MB827965).

Notes — *Lasiosphaeria miniovina* possesses the typical characters known for the genus: tomentose ascomata containing yellow centrum pigments (Miller & Huhndorf 2004a, b). This species can be distinguished by its small whitish ascomata, presence of a distinct ascal subapical globule, and short cylindrical ascospores that lack appendages and produce swollen heads with age. It has ascomata, asci and ascospores resembling *L. ovina*, but all characters are about half the size as those found in *L. ovina*. *Lasiosphaeria ovina* has ascospores with appendages but the ascospores never form a swollen head, whereas *L. miniovina* has ascospores that lack appendages and that form a swollen head with age. *Lasiosphaeria miniovina* is only known from Costa Rica, whereas *L. ovina* occurs widespread throughout north temperate regions, although it has been reported once from Costa Rica (as *Lasiosphaeria chrysentera*; Miller & Huhndorf 2004b). *Lasiosphaeria lanuginosa* occurs in Costa Rica and was collected at the same time (GenBank AY587916) as *L. miniovina*, but it differs in having longer ascospores (33–60 vs 22–33 µm) and ascospores with long, lash-like appendages.



Maximum likelihood tree generated using PhyML in Seaview v. 4.5.4 (Gouy et al. 2010). *Lasiosphaeria miniovina* is in **bold**. Numbers above branches refer to bootstrap support values. GenBank accession numbers for the ITS region are given after taxon names.

Colour illustrations. Background photo of typical tropical forest in Costa Rica; ascomata, longitudinal section through ascoma, longitudinal section through ascomal neck, longitudinal section through ascomal wall, ascus, paraphyses, ascospores and ascospore with swollen head. Scale bars = 500 µm (ascomata), 100 µm (ascomal sections), 10 µm (all others). Photos: Andrew N. Miller, Sabine M. Huhndorf, Gregory M. Mueller.

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Neocochlearomyces chromolaenae

Fungal Planet 851 – 14 December 2018

Neocochlearomyces Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous, *gen. nov.*

Etymology. Refers to its morphological similarity to *Cochlearomyces*.

Classification — *Muyocopronaceae*, *Muyocopronales*, *Dothideomycetes.*

Mycelium partly superficial and partly immersed, pale brown, smooth. *Conidiophores* solitary, macronematous, mononematous, subcylindrical, septate, erect, straight, brown, smooth, thick-walled, with basal rhizoids; stalk forming an apical fan-like conidiogenous region consisting of radiating brown, warty, septate, tightly aggregated cylindrical arms, with acute terminal cells. *Conidiogenous cells* terminal and intercalary on the one side of the swollen fan-like structure; loci inconspicuous, phialidic. *Conidia* falcate, aseptate, equilateral, with convex and flat plane, both ends obtuse to subobtusely rounded, hyaline, smooth-walled, guttulate, with a single, filiform, unbranched setula at each end on the inner straight plane, forming a slimy spore mass.

Type species. *Neocochlearomyces chromolaenae* Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous.

MycoBank MB828085.

Neocochlearomyces chromolaenae Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous, *sp. nov.*

Etymology. Name reflects the genus from which it was isolated, *Chromolaena*.

Conidiophores solitary, macronematous, mononematous, subcylindrical, unbranched, with 6–8 thickened transverse septa, erect, straight, brown, smooth, thick-walled, tapering slightly towards the apex, 7.5–12.5 µm diam at base, (90–)100–170 (–226) µm long, 3.5–5 µm diam at the apex, with basal rhizoids; stalk forming an apical fan-like conidiogenous region, 37.5–62.5 × 20–42.5 µm, consisting of radiating brown, warty, 3–5-septate, tightly aggregated cylindrical arms, with acute terminal cells. *Conidiogenous cells* terminal and intercalary on the one side of the swollen fan-like structure; loci inconspicuous, phialidic. *Conidia* 1.5–2.5 × 8.5–12.5 µm, falcate, aseptate, equilateral, with convex and flat plane, both ends obtuse to subobtusely rounded, hyaline, smooth-walled, guttulate, with a single, filiform, unbranched setula at each end, 3.8–5 µm long, on the inner straight plane, aggregating in mucoid droplet. *Sexual morph* unknown.

Culture characteristics — Colonies on PDA reaching 1.5 cm diam after 3 wk at 25 °C, effuse or punctiform, margins feathery, surface dark brown to black, reverse black. Fertile on PDA after incubation at 25 °C for 27 d.

Typus. Thailand, Nakhon Ratchasima, on leaves of *Chromolaena odorata*, 25 Sept. 2013, *U. Pinruan* (holotype BBH 41327, isotypes BBH 41328, 41329, culture ex-holotype BCC 68250, cultures ex-isotypes BCC 68251, 68252, ITS, LSU, SSU and *tef1* sequences GenBank MK047464.1–MK047466.1, MK047514.1–MK047516.1, MK047552.1–MK047554.1 and MK047573.1–MK047575.1, MycoBank MB828926).

Notes — Morphologically *Neocochlearomyces* differs from other known genera of hyphomycetes, being morphologically closest to *Cochlearomyces* (Crous et al. 2017b). It can easily be distinguished from the latter, however, as *Cochlearomyces* has synnemata with the swollen spoon-shaped conidiogenous region situated a third below the apex, and has conidia that are cylindrical, lacking setulae.

Colour illustrations. Chromolaena odorata in Nakhon Ratchasima province; fungus growing on host substrate; erect conidiophores, conidia, germinating conidium, colonies on PDA after 3 wk surface (left), and reverse (right). Scale bars morphological structures = 20 µm, Petri dishes = 1 mm.

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Ophiocordyceps houaynhangensis

Fungal Planet 852 – 14 December 2018

Ophiocordyceps houaynhangensis Keochanpheng, Thanakitp., Mongkols. & Luangsa-ard, *sp. nov.*

Etymology. Named after the place where the species was found – Houay Nhang Conservation Forest, Vientiane Province, Laos.

Classification — *Ophiocordycipitaceae*, *Hypocreales*, *Sordariomycetes.*

Stroma solitary, up to 11 cm long and 1.5–2.5 mm in width, cylindrical, cream; stipe simple. *Rhizoids* flexuous, arising from the head of *Coleoptera* larva, c. 2–6 cm long buried under the ground. Fertile part distinctly subterminal with asexual state at apex. *Ascomata* subterminal, cylindrical, pale yellow-brown with dark brown ostioles, 10–30 mm long, 2–3 mm in width. *Perithecia* completely immersed, obclavate, (300–)443–360(–450) × (80–)94–140(–170) µm. *Asci* cylindrical, (100–)115–207 (–250) × 4–5(–7.5) µm. *Ascospores* hyaline, cylindrical, breaking into 32 small truncate part-spores, (4–)5(–7) × 1–2 µm. *Asexual morph* terminal, whitish to pale yellow, up to 10 mm long, 0.5–1 mm in width. *Conidiogenous cells* monophialidic, phialides flask-shaped with long necks, up to 30 µm long and 2–4 µm in width; phialide necks up to 18 µm long and 0.5 µm in width. *Conidia* hyaline, smooth, spherical, 2–3 µm.

Culture characteristics — Colonies developed from germinating ascospores. The ascospores germinated within 24 h on PDA. Colonies on PDA moderately growing, c. 1 cm diam in 21 d at 25 °C. Colonies white, reverse pale brown. *Asexual morph* hirsutella-like, observed in some strains. Conidiogenous cells monophialidic, phialides (15–)18–26(–34) × 3–5 µm, necks present, (7–)9–16(–21) × 0.5 µm. Conidia, hyaline, smooth, spherical, 3–5 µm.

Typus. Laos, Vientiane Prov., Ban Danxang district, N18°05'28" E102°40'34", on *Coleoptera* larva, buried in soil, 31 Aug. 2016, *P. Nupason*, *K. Keochanpheng*, *JJ. Luangsa-ard*, *S. Mongkolsamrit*, *W. Noisripoom* & *D. Thanakitpipattana* (holotype BBH43166, culture ex-type TBRC8428, ITS, LSU and *tef1* sequences GenBank MH092891, MH092902 and MH092894, MycoBank MB825000).

Additional materials examined. Thailand, Saraburi Prov., Mueang Saraburi district, N14°31'33" E100°54'36", on *Coleoptera* larvae, buried in soil, 21 Sept. 2016, *JJ. Luangsa-ard*, *S. Mongkolsamrit* & *K. Keochanpheng*, BBH41960, BBC82809, ITS, LSU and *tef1* sequences GenBank MH092892, MH092908 and MH092899, BBH41961, BCC82810, ITS, LSU and *tef1* sequences GenBank MH092893, MH092909 and MH092900; Chiang Mai Prov., Ban Hua Thung district, N19°25'12" E98°58'15", on *Coleoptera* larvae, buried in soil, 5 Aug. 2015, *U. Pinruan*, *S. Preedanon*, *S. Sommai*, *P. Srikitikulchai*, *K. Tasanathai* & *S. Wongkanoun*, BBH41184, BCC78421, LSU and *tef1* sequences GenBank MH092904 and MH092897, BBH40264, BCC78167, LSU and *tef1* sequences GenBank MH092905 and MH092898.

Colour illustrations. Type locality – a trail in Houay Nhang Conservation Forest (photo by P. Nupason); stromata, fertile part with ascomata and asexual morph (arrow), perithecia, asci, ascus tip, part-spores, phialides, conidia, culture on PDA, asexual morph on PDA. Scale bars =10 mm (stromata), 100 µm (perithecia), 25 µm (asci), 10 µm (ascus tip and part-spores), 5 µm (phialides and conidia), 8 mm (plate culture), 5 µm (hirsutella-like morph on PDA).

Notes — *Ophiocordyceps houaynhangensis* produces ascomata on the subterminal part of the stroma, while the asexual morph is on the apex of the stroma, a feature reminiscent of *O. brunneipunctata* and *O. stylophora*. Their hosts are coleopteran larvae that can be found buried in soil. *Ophiocordyceps brunneipunctata* can be found throughout Thailand (Luangsa-ard et al. 2008) and Laos (our surveys and observation) while *Ophiocordyceps stylophora* is a rare species that was reported from North America (South Carolina; Minnessota) and China (Chachuła et al. 2011). Our phylogenetic analyses and morphological assessment support the placement of *O. houaynhangensis* in *Ophiocordycipitaceae* (Sung et al. 2007). Based on its micro-morphological characters, *O. houaynhangensis* more closely resembles *O. brunneipunctata* in the size of its part-spores that range from 4–6 × 1–1.5 µm (Hywel-Jones 1995, Evans et al. 2018), while *O. stylophora* produces whole ascospores, 102–164 × 2–3 µm (Mains 1958). However, *O. houaynhangensis* differs significantly from *O. brunneipunctata* in the size of perithecia and colour of its stroma as well as in the length of the phialides. In *O. houaynhangensis* the perithecia are longer than those reported for *O. brunneipunctata* (270–335 µm long) by Hywel-Jones (1995), and the stromata are pale yellow-brown with brown ostioles. In *O. brunneipunctata* they are cinnamon coloured, and the phialides are longer (up to 30 µm long) while they are shorter in *O. brunneipunctata* (up to 23 µm long). The results of our phylogenetic study using LSU and *tef1* sequences clearly separates *O. houaynhangensis* from *O. brunneipunctata*.

For supplementary information see MycoBank.

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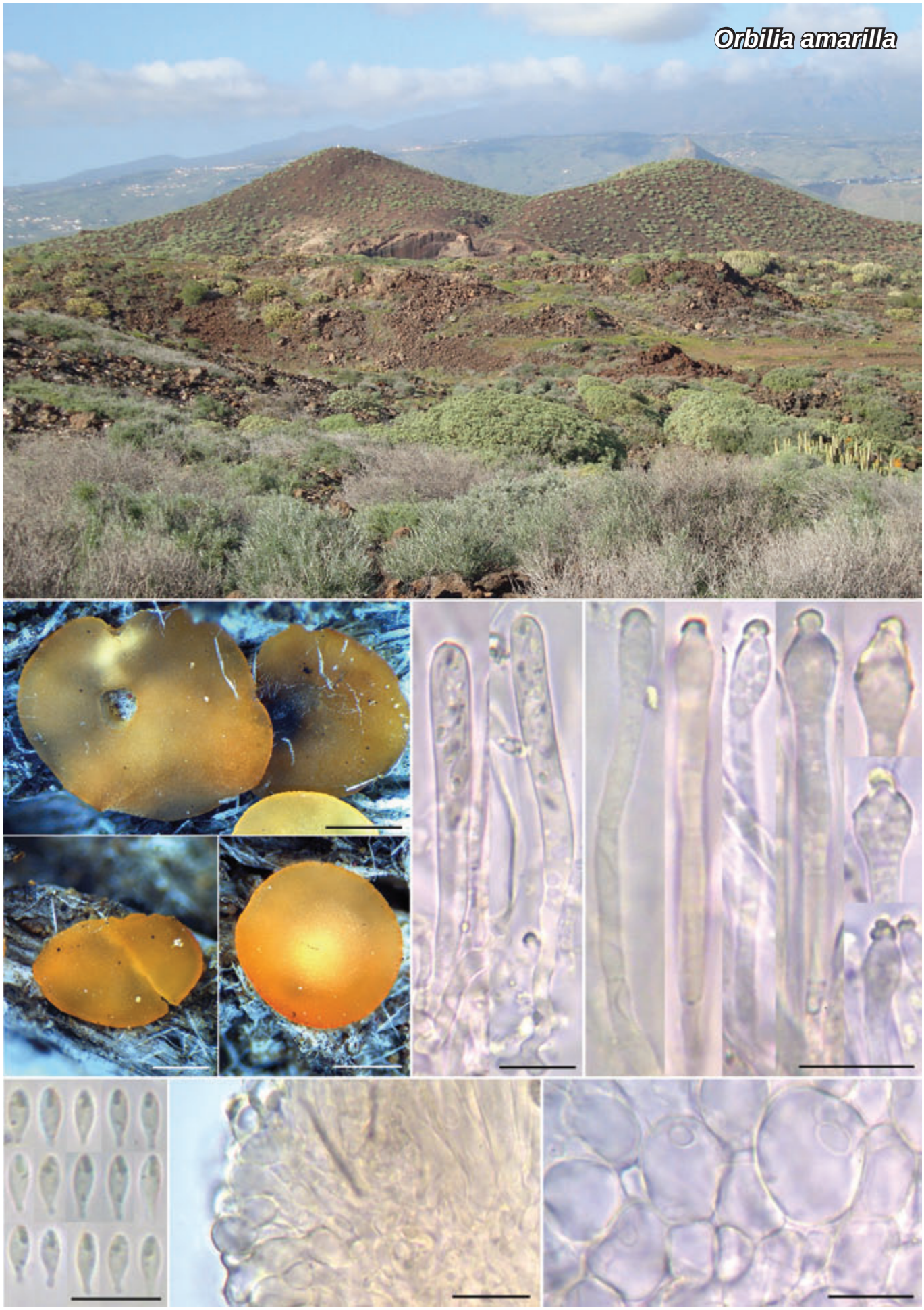

Orbilia amarilla

Fungal Planet 853 – 14 December 2018

Orbilia amarilla Quijada & Baral, *sp. nov.*

Etymology. Spanish: amarilla = yellow, after the yellow-orange apothecial colour, which coincides with the locality name Llanos de Amarilla.

Classification — *Orbiliaceae*, *Orbiliales*, *Orbiliomycetes.*

Apothecia rehydrated (0.5–)0.8–1.8 mm diam, to 0.2 mm high (receptacle 0.17 mm), bright orange-yellow to vivid orange, non-translucent, round to slightly undulating, scattered to subgregarious; disc slightly concave to slightly convex, margin smooth, 0–8 µm protruding; broadly sessile, superficial. *Asci* *(49.5–)53–58(–61) × 4.5–5.5 µm, †(36.5–)39–46(–52) × 3.4–4.3 µm, cylindrical-clavate, 8-spored, spores (obliquely) *2-seriate, 2–4(–6) lower spores inverted (usually mixed), pars sporifera *20–26 µm long; apex (†) strongly truncate (with a slight dent, laterally hardly inflated), hemispherical in profile view, thin-walled; base with medium to long, thin, flexuous stalk, L- to Y-shaped. *Ascospores* *(5.8–)6.4–7.3(–8) × (1.9–)2–2.2(–2.4) µm, †4.3–6.8 × 1.6–2 µm, fusoid to fusiform-clavate, straight, apex obtuse to subacute, base with a straight to slightly curved tail of *0.7–1.8 × 0.5–0.9 µm, sometimes slightly to distinctly bulbous at base; *SBs* *1.7–2.1 × 0.6–0.8(–1) µm, plug- to rod-shaped with a slightly bulbous base, straight to slightly, rarely medium bent, apically slightly widened and broadly attached at spore apex, often obliquely oriented. *Paraphyses* apically slightly to very strongly spathulate to mammiform, terminal cell *(10–)14–19(–22) × 2.5–4.5 µm, apical beak 1.3–1.7 × 1.7–2.2 µm (including exudate), exceeding the living asci by up to 3–7 µm, lower cells *(9–)10–13.3(–14.7) × 1.5–2.3(–3) µm, unbranched at upper septum, hymenium pale orange. *Medullary excipulum* very pale orange, 120 µm thick in centre, of loose to dense *textura intricata*(*-globulosa*), at flanks sharply delimited from ectal excipulum (partly by an indistinct ~5–10 µm thick layer of *textura porrecta*). *Ectal excipulum* from base to mid flanks of thin-walled, *textura globosa*, at flanks and margin light yellow-orange, 50 µm thick at base, cells *(8–)11–20(–23) × (7–)10–15(–17) µm, 25–35 µm thick at flanks, of vertically oriented *textura globulosa-angularis-prismatica*, cells *3.5–8.5 × 3.5–7 µm, at margin of 17 µm thick *textura prismatica-globulosa* oriented at 80°, marginal cortical cells *4–9 × 3–5 µm. Anchoring hyphae 2.5–5 µm wide, thin-walled, forming a rather dense *t. inricata-globulosa*. *VBs* often abundant in terminal cells of paraphyses, ± globose, medium refractive, hyaline. *SCBs* line- or ring-shaped, in lower cells of paraphyses and in ectal excipulum at lower flanks. *Exudate* over paraphyses 0.5–1 µm thick, cloddy to cap-like, individually firmly attached on beak and also sublaterally (beak seemingly thick-walled), pale yellow, at margin and flanks 1–1.5 µm thick, yellow-brownish. *Asexual morph*: unknown.

* = living state, † = dead state, VBs = vacuolar bodies, SCBs = KOH-soluble cytoplasmic bodies

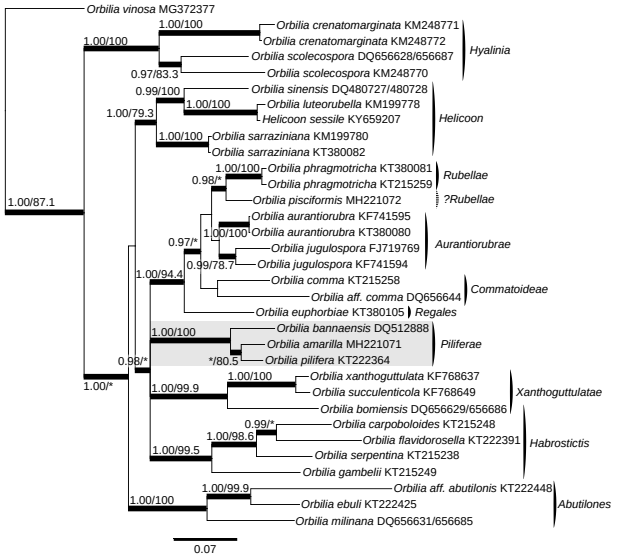
Colour illustrations. *Euphorbia* scrubs in Llanos de Amarilla; morphological features of *Orbilia amarilla*, from holotype, (top left to bottom right) fresh apothecia, living asci, living paraphyses (terminal cell with subglobose vacuolar bodies = VBs, lower cells with line-shaped KOH-sensitive cytoplasmic bodies = SCBs), living ascospores (with spore bodies = SBs), living excipular tissues in section, section at margin and section at base (cells with ring-shaped SCBs). Scale bars = 500 µm (apothecia), 10 µm (all others). All material mounted in H_2O.

Habitat — On superficially decayed, greyed wood of detached, branch of *Euphorbia canariensis* lying on the ground. Association: *Orbilia asomatica*, *O. beltraniae*, *O. pisciformis*. Desiccation tolerance: examined a few days after collecting in dry state, but certainly tolerant for several months.

Typus. Spain, Canary Islands, Tenerife, San Miguel de Abona, NE of Costa del Silencio, NNE of Monumento Natural de la Montaña Amarilla, N28°00'59" W16°38'03", 35 m alt., on detached branch of *Euphorbia canariensis* (*Euphorbiaceae*), 16 Dec. 2012, *L. Quijada & R. Castro* (holotype TFC Mic. 23767, ITS-LSU sequence GenBank MH221071, MycoBank MB825108).

Notes — *Orbilia amarilla* was collected on rotten wood of a detached, xeric branch of *Euphorbia canariensis* in the hyperarid *Euphorbia* scrubs in the south of Tenerife. In ascospore shape it resembles *O. pisciformis* (series *Commatoideae* or *Rubellae* ined.), which occurs in the same habitat, and *O. caudata* (series *Piliferae* ined.). These two species sharply differ, however, in having capitate paraphyses and partly glassy processes. Also, it resembles *O. pilifera* (series *Piliferae*), but this latter and *O. pisciformis* differ in having tear-shaped, narrowly attached spore bodies. A sequence of *O. amarilla* comprising SSU, ITS and LSU (S1506 intron absent) was obtained by Guy Marson (pers. comm.) from apothecia of the holotype. *Orbilia amarilla* shows an ITS distance of 7.5 % and LSU (D1–D2) distance of 3 % to *O. pilifera*, but 20 % (ITS) and 5.5 % (LSU) to *O. pisciformis*.

Our phylogenetical analyses supported the relationships between *O. amarilla* and *O. pilifera* in the clade of series *Piliferae* within sect. *Aurantiorubrae* of subg. *Habrostictis* (1.00 BIPP, 100 % ML-BS), see Baral et al. (2017).



Bayesian majority-rule consensus tree based on the ITS1-5.8S-ITS2 region of nrDNA. Thickened branches are those which were well supported by ML/BI methods (for Methods see Quijada et al. 2014). The eight different series of sect. *Aurantiorubrae* are indicated in the phylogenetic tree: here and also in the combined analysis in Baral et al. (2017), this section did not form a monophyletic clade with regard to sections *Helicoon* and *Habrostictis*. Asterisks (*) indicate a branch supported by only one of the two phylogenetic methods.

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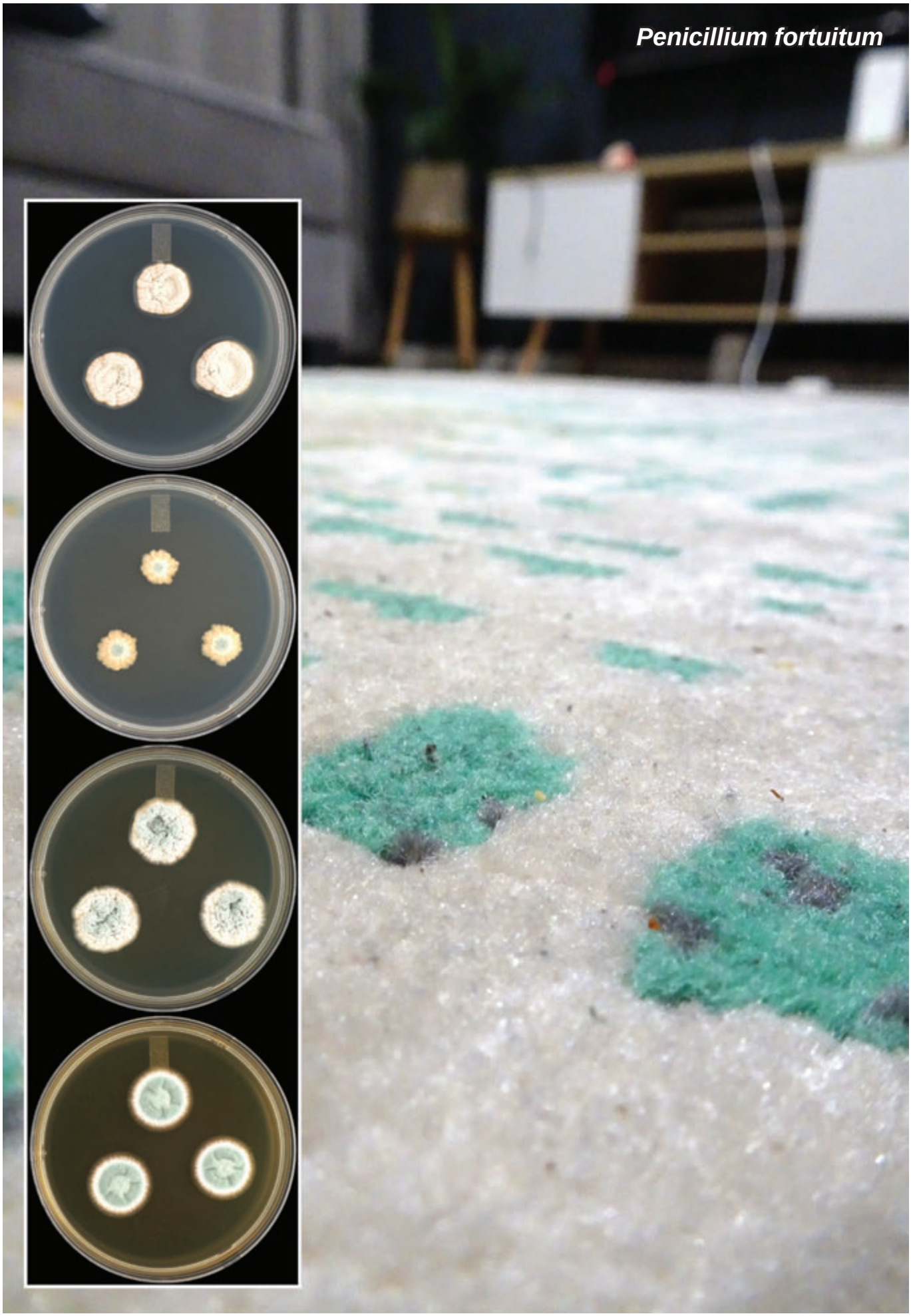

Penicillium fortuitum

Fungal Planet 854 – 14 December 2018

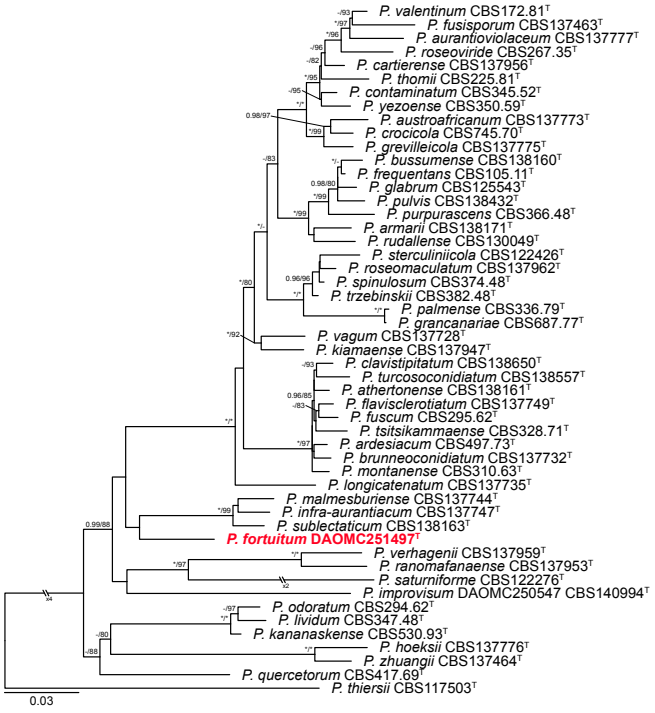
Penicillium fortuitum Visagie & Seifert, *sp. nov*.

Etymology. Latin, *fortuitum*, meaning fortuitous, named in reference to the new species having only one representative strain amongst ~2000 *Penicillium* strains isolated during this project.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores monoverticillate, minor proportion divaricate. *Stipes* smooth, (35–)50–130 × 2.5–3.5 µm. *Vesicle* 4–6(–7) µm. *Branches* two when present, 16–30 µm. *Phialides* ampulliform, 6–8 (rarely up to 16) per stipe/branch, 7.5–10 × 2.5–3.5 µm (av. 8.8 ± 0.8 × 3.1 ± 0.2). *Conidia* finely roughened, globose to subglobose, 3–4 × 2.5–3.5 µm (av. 3.3 ± 0.3 × 3.1 ± 0.2), average width/length = 0.94, n = 71.

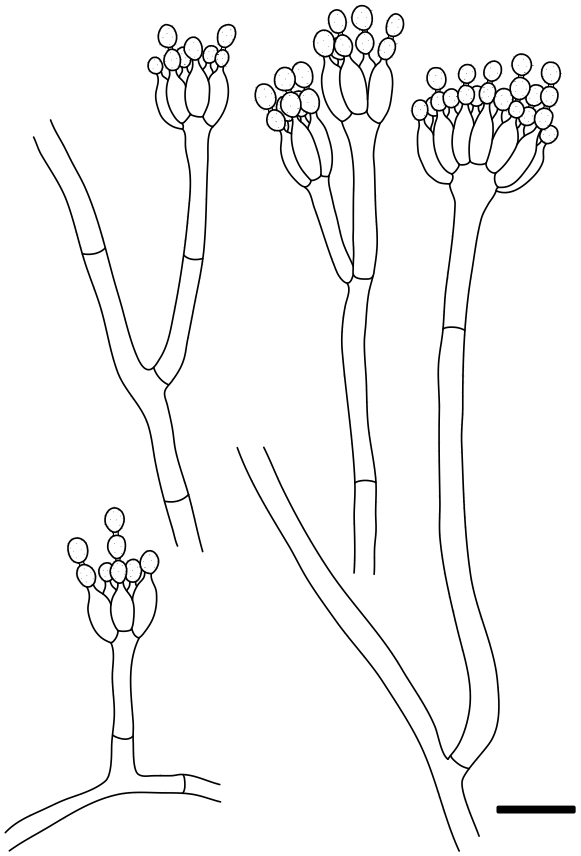
Culture characteristics (25 °C, 7 d) — *CYA*: Colonies moderately deep, randomly sulcate, sunken in at centre; margins moderately deep, somewhat irregular; mycelia white; texture floccose; sporulation dense, conidia *en masse* dull green (25D4–26D4), greenish grey (25B2); soluble pigments absent, sometimes brown; exudates absent; reverse brownish orange to light brown (6C7–7D8). *MEA*: Colonies low, raised centrally, sulcate; margins low, irregular; mycelia white; texture floccose; sporulation moderate, conidia *en masse* greyish green (25C5–D5); soluble pigments absent; exudates absent; reverse orange to light brown (6B8–7D8). *DG18*: Colonies similar colours to MEA, but faster growth and better sporulation. *YES*: Colonies similar to those on CYA, larger growth, reverse a deeper yellow (4A8) at centre. *CREA*: Growth moderate, no acid produced. Colony diam, after 7 d, in mm – CYA 15–19; CYA 37 °C no growth; CYA20S 19–20; MEA 14–15; MEA20S 22–26; DG18 14–18; YES 24–28; OA 17–18; MY1012 no growth; MY50G no growth; CREA 10–11.



Colour illustrations. Carpet inside home; colonies on CYA, MEA, YES and DG18.

Typus. USA, California, from house dust, 2009, coll. *A. Amend*, isol. *E. Whitfield & K. Mwange*, AA01US-904 = SLOAN 7240 (holotype DAOM 745786, cultures ex-type DAOMC 251497 = DTO 313-A3, ITS, *BenA* and *CaM* sequences GenBank MF803942, MF803836 and MF803932; MycoBank MB827860).

Notes — A BLAST search against an ex-type reference sequence dataset (Visagie et al. 2014b), placed the new species in *Penicillium* sect. *Aspergilloides*. A multigene phylogeny resolves *P. fortuitum* as sister to a clade containing *P. infra-aurantiacum*, *P. malmesburiense* and *P. sublectaticum*. Morphologically, it is easily distinguished from these based on its restricted growth on MEA, a character typical of *P. brunneoconidiatum*, *P. tsitsikammaense* and *P. turcosoconidiatum*. However, conidia of *P. brunneoconidiatum* have thick rough walls and are brown, colonies of *P. tsitsikammaense* typically produce sclerotia, while conidiophores of *P. turcosoconidiatum* have very short stipes (Houbraken et al. 2014).



Left: Combined phylogeny of sect. *Aspergilloides* based on ITS, *BenA* and *CaM*. Aligned datasets were analysed in IQ-tree v. 1.4 (Nguyen et al. 2015) and MrBayes v. 3.2.6 (Ronquist et al. 2012), with the tree obtained from the former shown. Bayesian posterior probabilities (≥ 0.95) and bootstrap support values (≥ 80 %) are given above the branches. The new species is indicated by **bold** red text, T = ex-type strain. The tree is rooted to *P. thiersii*. Alignments and trees can be accessed at TreeBASE (Submission ID 23322).
Above: Line drawing of *P. fortuitum* (DAOMC 251497T). Scale bar = 10 µm.

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Penicillium guaibinense

Fungal Planet 855 – 14 December 2018

Penicillium guaibinense J.P. Andrade, C.N. Figueiredo, R.P. Nascimento, P.A.S. Marbach, & J.T. De Souza, *sp. nov.*

Etymology. *guaibinense*, refers to Guaibim, an environmental protection area located in Bahia, Brazil, from where this species was collected.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores short and monoverticillate (83 % of the cases) and frequently occurring as side branches of the divaricate type of conidiophores, occasionally biverticillate (17 %). Isolated phialides born directly on hyphae occur frequently and mycelial coilings were sometimes observed. *Stipes* smooth to finely rough walled; monoverticillate stipes (6–)7–120(–170) × (1–)2–3(–4) µm. *Metulae* 1–2 per stipe of biverticillate conidiophores, (7–)8–14 × 2–3(–4) µm (av. 10.5 ± 2.3 × 2.6 ± 0.65). *Phialides* ampulliform, 1–6 per stipe, 4–8(–9) × (1–)2–3 µm (av. 5.9 ± 1.1 × 2 ± 0.26). Secondary elongated phialides resulting from percurrent proliferations were observed on approximately 10 % of the conidiophores (average of one secondary elongated phialide per conidiophore) on 7-d-old cultures grown on Blakeslee's Malt extract agar (MEAbl); these elongated phialides measured (6–)11–24 × 1.5–2 (av. 14.8 ± 6 × 1.8 ± 0.26). *Conidia* finely rough, broadly subglobose, 2–3 × 2–3 µm (av. 2.3 ± 0.37 × 2.2 ± 0.32), average width/length = 0.98 ± 0.03, n = 78.

Culture characteristics — Colony diam, 7 d, in mm: Czapek Yeast Autolysate agar (CYA) 27–31; CYA 30 °C (20–)36–38; CYA 37 °C 26–28(–36); CYA 5 °C no growth; MEAbl 25–28; Yeast extract sucrose agar (YES) 21–25; Dichloran 18 % Glycerol agar (DG18) 18–20; Czapek Yeast Autolysate agar with 5 % NaCl (CYAS) 16–17; Oatmeal agar (OA) 34–40; Czapek's agar (CZ) (21–)27–32; Creatine sucrose agar (CREA) 20–23, acid production absent.

CYA, 25 °C: Colonies moderately deep, radially and concentrically sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate; conidia *en masse* pale yellow, grey to greenish grey (1A3–B1–1C2–D2); exudate clear and soluble pigment bright yellow sometimes present; reverse dull yellow, greyish yellow to greyish orange (3B3–B4–4B6–5B5) at centre and dull yellow to greyish green (3B3–28B3) at margin. MEAbl, 25 °C: Colonies raised in the centre and sometimes radially and concentrically sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* pastel yellow to grey (1A4–2C1); exudate clear, sometimes present, soluble pigment absent; reverse olive yellow, greyish orange to brownish orange (3C6–D6–5B5–6C7), light yellow (4A5) at centre and greyish yellow (4B3–B4) at margin. YES, 25 °C: Colonies moderately deep, radially, concentrically and randomly sulcate, margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* grey (2C1–D1); exudate absent, soluble pigment absent; reverse greyish yellow (4B6) at centre and greyish yellow (4A4–B4–B3–C3) at margin. DG18, 25 °C: Colonies moderately deep, radially sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to dense, conidia *en masse* greyish yellow, greenish grey to greyish green (1B4–1C2–1D3); exudate absent, soluble pigment yellow, sometimes present; reverse greenish yellow to greyish yellow (1A7–1B6) at centre and pale yellow (1A3) at margin. CYAS, 25 °C: Colonies moderately deep, randomly sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate; conidia *en masse* pale yellow to grey (2A3–B1–C1); exudate absent, soluble pigment bright yellow; reverse greyish yellow (2B4–4C6) at centre and yellowish white (2A2) at margin. OA, 25 °C: Colonies low, plane; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* brownish grey (5C2); exudate clear, sometimes present, soluble pigment yellow; reverse greyish yellow (3C5–4C7) at centre and dull yellow to greyish yellow (3B4–C3–C4) at margin. CZ, 25 °C: Colonies low, plane; margins low, narrow, irregular to entire; mycelia white; texture floccose; sporulation absent to sparse, conidia *en masse* yellowish white to greenish grey (1A2–1B2); exudate absent, soluble pigment absent; reverse white to yellowish white (1A1–A2).

Colour illustrations. Guaibim environmental protection area located in Bahia, Brazil; 7-d-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbl, YES and OA; bottom row left to right, reverse CYA, MEAbl, YES and obverse CREA, conidiophores with elongated secondary phialides, phialides born directly on hyphae, conidiophores, coiling of mycelia and conidia. Scale bars = 10 µm.

Typus. Brazil, Bahia, in soil from the Guaibim sandbank, S13°18' W38°57', 5 Nov. 2011, *J.P. Andrade* (holotype HURB 18573 (dried culture on MEA); culture ex-type CCDCA 11512 = 23EM8, ITS, *BenA* and *CaM* sequences GenBank MH674389, MH674391 and MH674393, MycoBank MB827182).

Additional materials examined. Brazil, Bahia, in soil from the Guaibim sandbank, CCDCA 11510 = 23EM7, 30 Oct. 2011, *J.P. Andrade*, ITS, *BenA* and *CaM* sequences GenBank MH674390, MH674392 and MH674394; ibid., 2 Dec. 2011, *J.P. Andrade*, 67M4 and 67EM8.

Notes — *Penicillium guaibinense* morphologically resembles *P. curticaule* (Visagie et al. 2015) and is phylogenetically more related to *P. singorense* (Visagie et al. 2014a), both included in sect. *Lanata-Divaricata*. However, comparisons of ITS, *BenA* and *CaM* revealed that it differs from *P. singorense* by six transitions in *BenA* and nine in *CaM*, three transversions in *BenA* and six in *CaM*, one indel in each of these genes, and by one transition in ITS (TreeBASE submission ID 23052). The differences between *P. guaibinense* and its closest related species, *P. singorense*, are larger than the differences between other described species in sect. *Lanata-Divaricata*, such as *P. coerulum* and *P. levitum* (Visagie et al. 2014a). *Penicillium guaibinense* grows slower than *P. singorense* on all media and temperatures tested, but it grows faster than *P. curticaule* on CYA 37 °C, CYAS and OA. *Penicillium guaibinense* may produce a soluble bright yellow pigment in CYA and secondary elongated phialides in ± 10 % of the conidiophores, both of these characteristics were not reported for *P. singorense* and *P. curticaule*. *Penicillium guaibinense* has shorter stipes than *P. singorense* and longer stipes than *P. curticaule*. *Penicillium guaibinense* produces mycelial coils similar to *P. curticaule*, but these structures were not reported for *P. singorense*. All macroscopic and microscopic measurements were done twice, independently, for isolates CCDCA 11512 and CCDCA 11510.

For supplementary information see MycoBank.

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Periconia caespitosa

Fungal Planet 856 – 14 December 2018

Periconia caespitosa Cantillo, Gusmão & Madrid, *sp. nov.*

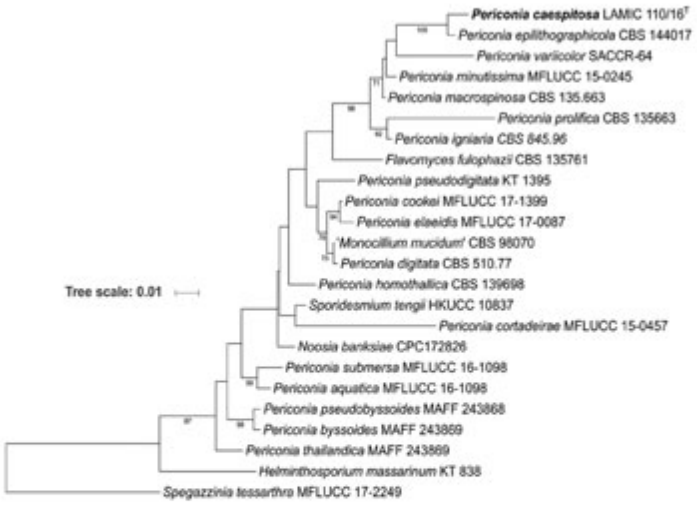
Etymology. Named after its conidiophores that developed in tufts or dense patches.

Classification — *Periconiaceae*, *Pleosporales*, *Dothideomycetes.*

On natural substrate. *Colonies* on decaying leaves dark brown to black, producing a reddish pigment. *Mycelium* immersed in the substrate, composed of septate, pale brown to subhyaline, smooth, 3.5–4 µm wide hyphae. *Conidiophores* macronematous, mononematous, septate, unbranched or rarely branched, caespitose, straight to flexuous, setiform and sometimes uncinated at the tip, pale brown at the base, brown towards the apex, minutely roughened at the base and at the apex, as well as in the areas nearest of conidiogenous cells, otherwise smooth, up to 500 µm long, 5–6 µm wide at the base, fertile at the lower-median part and sometimes also at the apex. *Conidiogenous cells* polyblastic, pale brown, finely roughened, intercalary and terminal, globose, subglobose or obpyriform (6–)7.5–9 × 6.5–7.5 µm. *Conidia* globose, aseptate, reddish brown, thick walled, dry, solitary or in short basipetal chains of 2–4 conidia, (6–)6.5–9 µm diam, strongly echinulate, spines 1–1.5 µm long, maturation basipetal. *Secession* schizolytic. *Sexual morph* not observed.

Culture characteristics — *Colonies* cottony, fast growing, with regular edges, attaining 90 mm diam after 6 d on PDA and CMA at 25 °C, hyaline hyphae on vegetative mycelium, aerial mycelium rosaceous white with white reverse on PDA, dark green to olivaceous green with blackish green reverse on CMA; diffusible pigments absent in both culture media. Conidiophores same as in natural substrate but more frequently branched and fertile at tips.

Typus. Brazil, Ceará, Missão Velha Waterfall Geosite, on decaying leaves of unidentified dicotyledonous plant, 30 Apr. 2016, *T. Cantillo* (holotype HUEFS 239357, culture ex-type LAMIC 110/16, ITS and LSU sequences GenBank MH051906 and MH051907, MycoBank MB827635).



Colour illustrations. Missão Velha Waterfall Geosite, Ceará state (photo by M.O. Marques); conidia, conidiogenous cells and conidiophores from type, colonies on PDA (top) and CMA (bottom) and colonies on natural substrate with a reddish pigment. Scale bars = 50 µm (conidiophores), 10 µm (conidiogenous cells and conidia).

Notes — BLAST searches indicated that the closest relative of *Periconia caespitosa* represented in GenBank is *P. epilithographicola* CBS 144017 (ITS GenBank MF422162, Identities = 578/590 (98 %), 4 gaps (0 %)). Both species have finely roughened conidiogenous cells, produce reddish pigment, and have a similar conidial size; but, on PDA, *P. epilithographicola* has creeping hyphae and greyish to black conidiophores forming small agglutinated, black, sticky drop-like structures instead of caespitose, brown and setiform conidiophores with dry conidia in short chains, as occurs with *P. caespitosa*. These species clustered together with a maximum-likelihood bootstrap support value of 100 % but no LSU sequences of *P. epilithographicola* are available for comparison and therefore a phylogenetic analysis could not be performed. Given the morphological and cultural differences and also the low clustering quality values produced by both genetic markers at the generic level, we consider *P. caespitosa* as a new species. In addition, *P. caespitosa* is morphologically different from all currently accepted *Periconia* species (Subramanian 1955, Rao & Rao 1964, Ellis 1971, 1976, Cantrell et al. 2007, Markovskaja & Kačergius 2014, Tanaka et al. 2015, Wu et al. 2015, Liu et al. 2017, Coronado-Ruiz et al. 2018, Crous et al. 2018b, Vu et al. 2019). Among all the species of *Periconia* with clustered conidiophores the most similar to *P. caespitosa* are *P. clitoriae*, *P. tirupatiensis*, *P. saraswatipurensis* and *P. atropurpurea*, but these can be differentiated from *P. caespitosa* by the combination of features such as the aggrupation of conidiophores and the position of conidiogenous cells in them, conidial size and ornamentation, and pigment production on natural substrates and/or in culture. The most similar species to *P. caespitosa* is *P. clitoriae*, whose conidiophores arise in dense clusters and conidiogenous cells are located laterally at the upper three cells or at apex. Also, conidia of *P. clitoriae* are slightly bigger (8.5–9.5 µm diam) and also distinctly verrucose (Subramanian 1955) whereas in *P. caespitosa* conidia are echinulate; in addition, lateral conidiogenous cells in *P. caespitosa* are located in the lower portion of the conidiophore and sometimes terminally. Unfortunately, no DNA sequence data of *P. clitoriae* is available in GenBank for comparison.

Maximum Likelihood (ML) tree inferred from ITS-LSU nrDNA sequences. Phylogenetic analyses were performed with MEGA v. 7 (Kumar et al. 2016), with the best DNA substitution model determined by the same software. Statistical support was determined by bootstrap analysis of 1 000 replicates. Bootstrap support values ≥ 70 % are depicted at the internodes. *Periconia caespitosa* is marked in **bold** face.

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Phaeotheca shathenatiana

Fungal Planet 857 – 14 December 2018

Phaeothecaceae B.A. Darveaux, *fam. nov*.

Classification — *Phaeothecaceae*, *Capnodiales*, *Dothideomycetes*.

MycoBank MB828184.

Mycelium consisting of hyaline to brown, smooth-walled, septate, branched hyphae, that swell up in terminal or intercalary cells, and develop numerous endoconidia. Endoconidia brown, smooth to verruculose, thin- to thick-walled, globose to obovoid, aseptate to muriformly septate.

Type genus. Phaeotheca Sigler et al.
MycoBank MB9323.

Note — The family *Phaeothecaceae* presently only includes *Phaeotheca*, based on *P. fissurella*.

Phaeotheca shathenatiana B.A. Darveaux, *sp. nov.*

Etymology. From the first three letters of my children's names, Shawn, Theresa and Natalie.

Microscopic characteristics on 2 % malt extract agar: *Hyphae* brown, smooth, thin-walled, 10–20 × 3–4 µm. *Conidiophores* absent. *Conidiogenous cells* integrated, vegetative hyphae cells become conidiogenous, brown, 15–25 × 3–5 µm, expanding to 20–30 × 15–30 µm as endoconidia develop, enlarging as the cytoplasm compartmentalizes, one endoconidium forms from each compartment, successive enlarged cells resemble sausages, often one large cell that has ruptured or is near rupturing, bracketed by 3–5 lesser enlarged cells on both sides, mature conidiogenous cell finally ruptures and releases mature endoconidia. *Conidia* endogenous, unicellular, brown when seen *en masse*, pale brown when viewed individually, thin-walled, smooth, irregularly angular, especially when recently released, due to being pressed together in the conidiogenous cell, later becoming globose to subglobose, becoming less angular as they get older after release, 4–6(–7) µm diam, 5–30 per conidiogenous cell. *Secondary conidia* none.

Culture characteristics (2 % malt extract agar) — Very slow growth, colony diameter increase is 2–4 mm/wk (27 °C) eventually stopping, not covering plate. Mycelium dense, growing edge sharp, aerial hyphae developing just behind slowly advancing submerged hyphae, aerial hyphae on older areas, exudate droplets on surface containing conidia, centre of colony becoming raised. Colour dark brown to black, reverse black.

Typus. USA, Alaska, Anchorage, from twig and cone litter, 30 Sept. 1997, coll. *D. Duffy*, isol. *B.A. Darveaux*, on 2 Oct. 1997, MSX102094 (holotype SYRF0012523, permanently preserved on microscope slide), isotypes NY03304532, BPI 910718, DAOM836219, DUKE0351831, permanently preserved on microscope slides; ITS sequences GenBank MH745097 and MH745098, LSU sequence GenBank MH745096, MycoBank MB826890.

Colour illustrations. Twig and cone litter; MSX102094 colony sporulating on 2 % malt extract agar showing integrated conidiogenous cells swelling, compartmentalising, and rupturing to release endospores (inset), sausage-like appearance of conidiogenous cell development and rupture (bottom photo). Scale bars = 10 µm. Photos: Blaise A. Darveaux.

Notes — The current fungus shares generic diagnostic features of *Phaeotheca* such as predominant endogenous conidiogenesis, slow restricted growth at room temperature, and angular brown conidia (Sigler et al. 1981.) However, *P. shathenatiana* differs from the other four species of the genus by: *P. fissurella* usually has 1–3 (rarely more) endoconidia per conidiogenious cell (Sigler et al. 1981); *P. dimorphospora* forms hyaline, cylindrical secondary conidia from primary endocondia (DesRochers & Ouellette 1994); *P. triangularis* and *P. salicorniae* both produce septate endoconidia (De Hoog et al. 1997, Crous et al. 2016b).

Our phylogenetic analysis using partial LSU sequence data along with described species of *Phaeotheca* including members of asexual *Capnodiales* from an alignment published by Bose et al. (2014), shows strain *P. shathenatiana* clusters with the type species *P. fissurella* as a strongly supported clade (91 % RAxML bootstrap support). Our analysis also shows that *Phaeotheca* is a polyphyletic genus consistent with conclusions drawn in previous studies (Crous et al. 2016b). *Phaeotheca* represents an undescribed, monotypic family in *Capnodiales*, for which *Phaeothecaceae* is herewith introduced.

There are many other genera that produce endoconidia, usually to a minor extent, but relatively few rely on this mode as their main form of conidiogenesis. Several genera of the latter type are *Coccidioides*, *Phaeothecoidea*, *Endoconidioma* and *Hyphospora* (Seifert et al. 2011.)

Endospores of *Coccidioides* come from sphaerules rather than intercalary hyphal cells and it has alternate-arthric conidia which *P. shathenatica* does not have (Seifert et al. 2011).

Phaeothecoidea differs in that the endoconidia are verruculose, 1–2-septate, and give rise to additional endoconidia. However, the photomicrographs of *Phaeothecoidea melaleuca* look very similar to the current fungus (Crous et al. 2010).

Endoconidioma differs in that it has a pycnidium-like conidiomata and solitary blastoconidia. Seifert et al. (2011) considers *Endoconidioma* a coelomycete.

Hyphospora differs in that it has hyaline mycelium and conidia and a depressed hemispheric central part of the colony surrounded by a halo of hyaline hyphae in the agar (Ramaley 1996).

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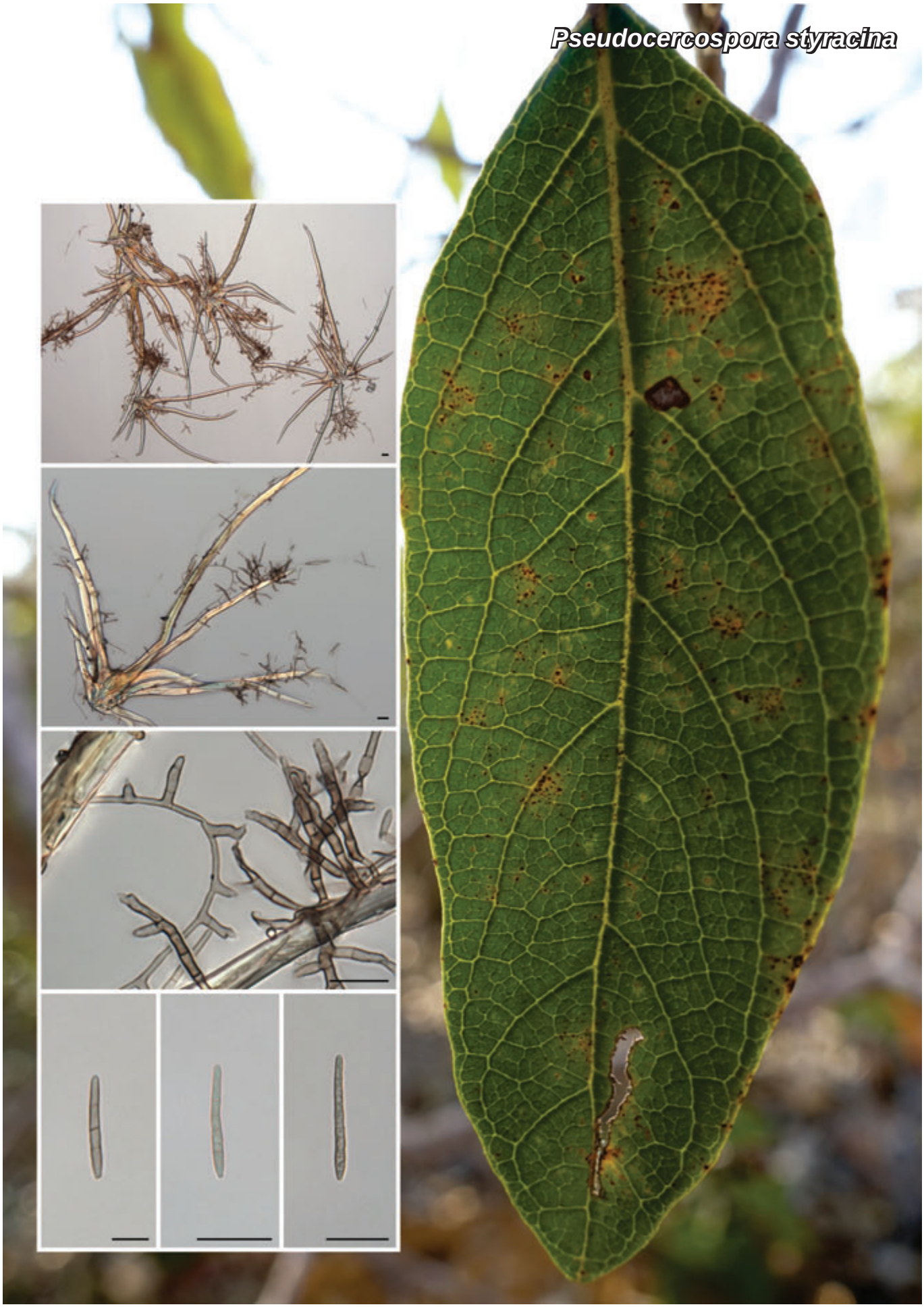

Pseudocercospora styracina

Fungal Planet 858 – 14 December 2018

Pseudocercospora styracina V.P. Abreu & O.L. Pereira, *sp. nov*.

Etymology. Name derived from its host genus, *Styrax*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

Leaf spots amphigenous, circular to irregular, initially chlorotic, becoming brown with age, 4–10 mm diam. *Internal mycelium* indistinct. *External mycelium* brown, septate, branched, smooth, 1.5–2.5 µm diam, colonising the trichomes. *Stromata* absent. *Conidiophores* hypophyllous, cylindrical, branched, solitary, 19–57 × 2–4.5 µm, 1–7-septate, straight or geniculate, brown, smooth, sometimes restricted to conidiogenous cells. *Conidiogenous cells* terminal, 7–13.5 × 2.5–4.5 µm, or conidiophores reduced to conidiogenous cells, 3.5–12.5 × 2–4 µm, subcylindrical, brown, smooth, proliferating sympodially. *Conidiogenous loci* inconspicuous, unthickened, not darkened. *Conidia* solitary, guttulate, pale brown to brown, smooth, subcylindrical, straight to slightly curved, 22.5–47.5 × 2–3 µm, base truncate, 1–3-septate, hila neither unthickened nor darkened, 1–1.5 µm diam.

Culture characteristics — Colonies on PDA 34 mm diam after 20 d at 25 °C with a photoperiod of 12 h; with aerial mycelium sparse, grey, reverse iron-grey, sterile.

Typus. Brazil, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA-Paraopeba), on leaves of *Styrax* sp. (*Styracaceae*), 1 July 2015, *O.L. Pereira* (holotype VIC 44382, culture ex-type COAD 2369; ITS, LSU, *tef1* and *actA* sequences GenBank MH397664, MH480643, MH480642 and MH480641, MycoBank MB824660).

Notes — Cercosporoid fungi include several genera of microfungi with cosmopolitan distribution and are highly diverse especially in tropical and subtropical countries (Crous et al. 2013, Bakhshi et al. 2014, Silva et al. 2016). *Pseudocercospora* species can be found as saprobes, endophytes, hyperparasites, being very common as plant pathogens – causing mainly leaf spots (Crous et al. 2013, Braun et al. 2016, Guatimosim et al. 2016). Cercosporoid fungi have been reported as host-specific (Guatimosim et al. 2016, Silva et al. 2016). Four cercosporoid fungi have been described from *Styrax* spp.: *Passalora styracis*, *Cercospora apii* s.lat. (= *Cercospora styracicola*), *Pseudocercospora fukuokaensis* and *Cercoramularia koreana* (Crous & Braun 2003, Videira et al. 2017). Morphologically, *P. styracina* clearly differs from *P. fukuokaensis* and *P. brackenicola* by having external mycelium colonising the trichomes and stromata absent. Additionally, the conidia length of *P. styracina* (22.5–47.5 µm) are shorter than *P. fukuokaensis* (30–70 µm) and *P. brackenicola* (20–77 µm) (Chupp 1954, Guatimosim et al. 2016). *Pseudocercospora styracina* does not correspond to any sequence available in GenBank at present. Hence, it is described here as a new species.

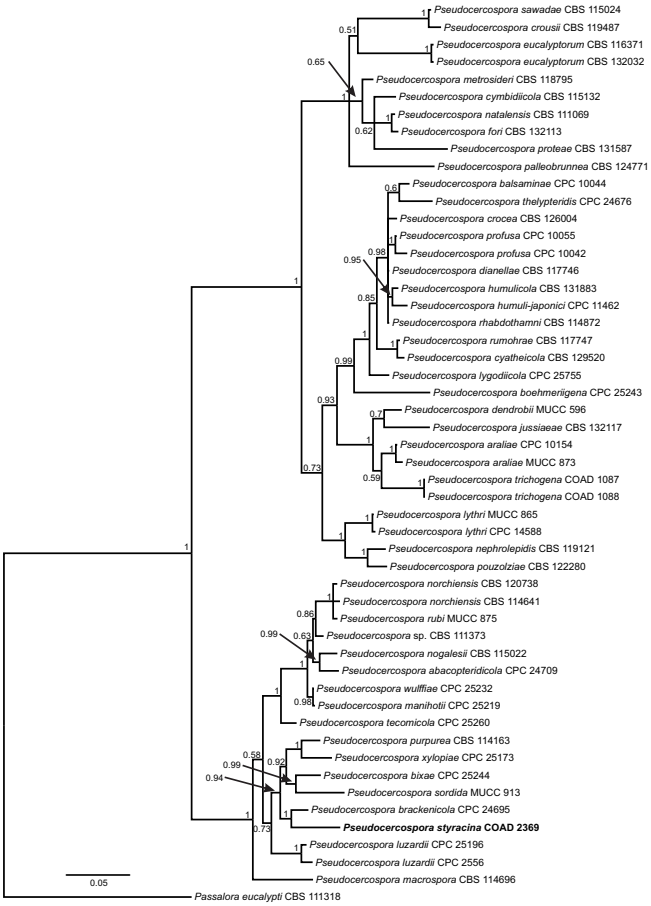
Based on a megablast search of NCBIs GenBank nucleotide database, the ITS sequence is identical to *P. norchiensis* (GenBank MF663573), *P. brackenicola* (GenBank NR_147290) and *P. abacopteridicola* (GenBank KT037518).

Colour illustrations. Chlorotic leaf spots symptoms on *Styrax* sp. (*Styracaceae*) in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; external mycelium with conidiophores and conidiogenous cells colonising the trichomes and pigmented conidia with inconspicuous, unthickened, not darkened conidiogenous loci. Scale bars = 20 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the LSU sequence is identical to *P. brackenicola* (GenBank KT037565), *P. tecomicola* (GenBank KT290183) and *P. bixae* (GenBank KT290180).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *tef1* sequence are *P. brackenicola* (GenBank KT037484; Identities = 470/504 (93 %), 7 gaps (1 %)), *P. bixae* (GenBank KT290207; Identities = 457/501 (91 %), 2 gaps (0 %)) and *P. luzardii* (GenBank KT290194; Identities = 462/511 (90 %), 10 gaps (1 %)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *actA* sequence are *P. macrospora* (GenBank GU320447; Identities = 154/163 (94 %), no gaps), *P. luzardii* (GenBank GU320440; Identities = 154/164 (94 %), 1 gap (0 %)) and *P. purpurea* (GenBank GU320486; Identities = 153/164 (93 %), no gaps).



Bayesian inference tree obtained by phylogenetic analyses of the combined ITS, *actA* and *tef1* sequences conducted in MrBayes on XSEDE at the CIPRES Science Gateway (Miller et al. 2010). Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold** face. *Passalora eucalypti* (CBS 111318) was used as outgroup.

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Pseudopenidiella gallaica

Fungal Planet 859 – 14 December 2018

Pseudopenidiella gallaica Iturrieta-González, Dania García, Gené, *sp. nov.*

Etymology. Name refers to the Spanish region where the species was collected.

Classification — *Microthyriaceae*, *Microthyriales*, *Dothideomycetes.*

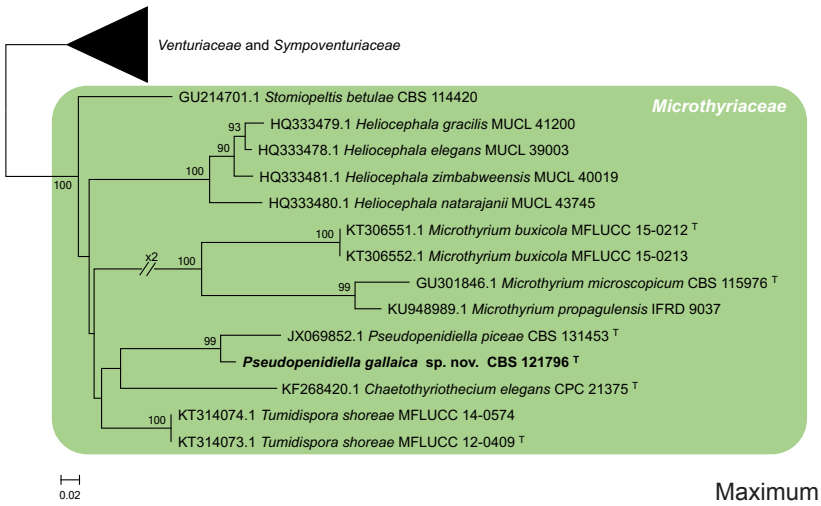
Mycelium consisting of branched, septate, pale brown, smooth-walled to verruculose hyphae of 1–1.5 µm diam. *Conidiophores* mononematous, dimorphic: microconidiophores reduced to conidiogenous cells on hyphae, 13–19 µm high, apex truncate 2 µm wide, pale brown; macroconidiophores unbranched, erect, subcylindrical, with up to 3-septate, pale brown to brown, often verruculose towards the apex, smooth- and thick-walled towards an often swollen base, up to 55 µm long (up to 120 µm long on the natural substratum), 2–3 µm wide. *Conidiogenous cells* terminal or subterminal, mono- or polyblastic, with up to 4 inconspicuous conidiogenous loci, verruculose, pale brown, 11–21.5 × 1.5–3 µm. *Ramoconidia* subcylindrical, aseptate, pale brown, smooth to verruculose, 7.5–11 × 2–3 µm, forming conidia in acropetal branched chains. *Conidia* cylindrical to ellipsoidal, aseptate, pale brown, smooth-walled to verruculose, 6–12 × 1–3 µm. *Sexual morph* not observed.

Culture characteristics — Colonies on PDA reaching 8–9 mm diam after 30 d at 25 °C, golden grey to black, velvety, erumpent, aerial mycelium scarce,feathery margin; reverse dark brown to black. On OA reaching 5–6 mm diam after 30 d at 25 °C, olive brown to black, slightly dusty, flat, aerial mycelium scarce; reverse dark brown to black.

Typus. Spain, Galicia, Pontevedra, Natural Park of Monte Aloia, on unidentified dead leaves, Feb. 2006, *J. Mena & C. Silvera* (holotype FMR H-9234, cultures ex-type CBS 121796 = FMR 9234; ITS and LSU sequences GenBank LT984842 and LT984843, MycoBank MB828082).

Notes — *Pseudopenidiella* was introduced to accommodate *P. piceae* (Crous et al. 2012b), a hyphomycetous fungus morphologically similar to *Cladosporium*, but phylogenetically distant to the family *Cladosporiaceae* (*Capnodiales*, *Dothideomycetes*). The genus was characterised by the formation of dimorphic conidiophores with terminal aseptate ramoconidia producing branched conidial chains, and by the absence of coronate-type scars on conidia or conidiogenous cells. In addition to the type, *P. pini* (formerly *Polyscytalum pini*; Kirk 1983) is currently included in *Pseudopenidiella* (Kirk 2014). However, the phylogeny of this latter species is obscure since only herbarium material (holotype IMI 242163) is available for comparison. *Pseudopenidiella pini* is characterised by the production of short and broad denticulate conidiogenous cells, a feature not described in *Pseudopenidiella*. *Pseudopenidiella gallaica* differs from *P. piceae* in its shorter conidiophores (up to 55 µm long in culture – up to 120 µm on the natural substratum – vs 150 µm long in *P. piceae*) and slightly longer conidia (up to 12 µm in *P. gallaica* vs up to 10 µm in *P. piceae*).

Based on a megablast search of NCBIs GenBank nucleotide, LSU sequence of *P. gallaica* showed a similarity of 95 % (742/785) with that of *P. piceae* (CBS 131453, GenBank NG_042681); while ITS sequence did not reveal any close hits. Our phylogenetic reconstruction shows that *Pseudopenidiella* is related to the members of the family *Microthyriaceae* (Abarca et al. 2011, Singtripop et al. 2016).



Maximum likelihood tree obtained from the analysis of LSU sequences of *Pseudopenidiella* and related genera of the family *Microthyriaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 555 bp and was performed with ClustalW. Tamura Nei with Gamma distribution (G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold** face. A superscript T denotes ex-type cultures.

Colour illustrations. Natural Park of Monte Aloia, Pontevedra, Galicia, Spain; colony sporulating on PDA after 30 d at 25 °C and conidia after 10 d at 25 °C. Scale bars = 10 mm (colony) and = 10 µm (microscopic structures).

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Pseudopyricularia persiana

Fungal Planet 860 – 14 December 2018

Pseudopyricularia persiana G. Ghorbani, Pordel & Jav.-Nikkh., *sp. nov.*

Etymology. Name refers to the old name of Iran, Persia.

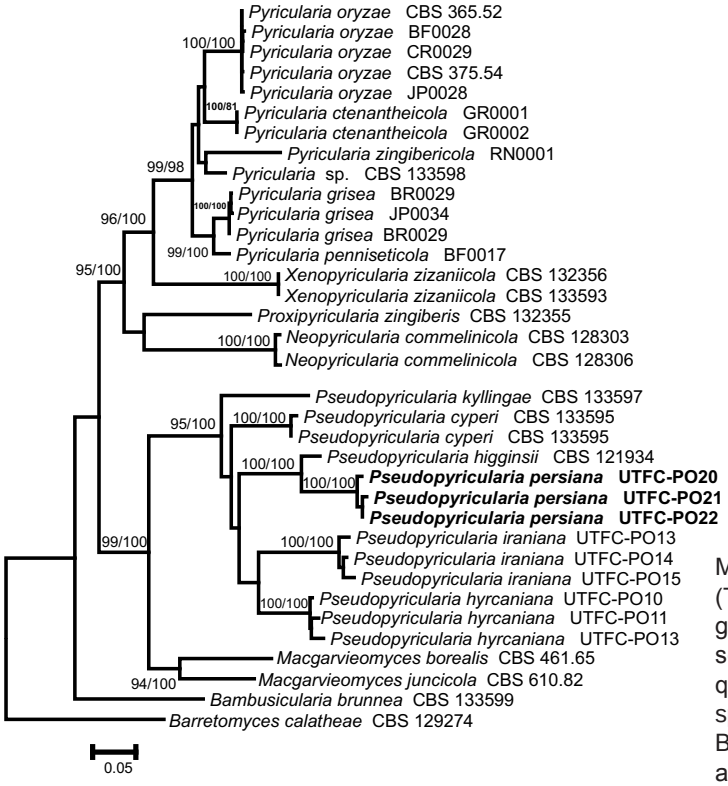
Classification — *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetes*.

Mycelium on SNA, and OA, consisting of smooth, hyaline, branched, septate hyphae. *Conidiophores* scattered, solitary, erect, pale brown, swollen at the base, macronematous, mononematous, typically unbranched, rarely branched, straight, aseptate, some conidiophores consisting of 1–6 cells, 137–332(–380) × 5–7 µm. *Conidiogenous cells* integrated, terminal, intercalary, sympodial, cylindrical, geniculate, denticulate; denticles cylindrical, thin-walled, pale brown. *Conidia* solitary, dry, obclavate, hyaline, (30–)36–52(–65) × 10–13 µm, 2(–3)-septate, hilum often protuberant, conidia produce secondary conidiophore. *Sexual morph* unknown.

Culture characteristics — Colonies on OA transparent, buff, reaching 42 mm diam after 1 wk at 23–25 °C; on PDA transparent, white, and straw reverse, reaching 26 mm diam after 1 wk at 23–25 °C.

Typus. Iran, Guilan province, Lasht-e Nesha city, on infected leaves of *Cyperus* sp., 19 Oct. 2017, *G. Ghorbani* (holotype UTFC-PO20, culture ex-type UTFC-PO21, ITS, LSU, *RPB1* and *CAL* sequences GenBank MH780926, MH780974, MH699975 and MH699978, MycoBank MB826968).

Notes — This species is similar to *Ps. higginsii*, *Ps. cyperi*, *Ps. iraniana*, *Ps. kyllingae* and *Ps. hagahagae* in having 2-septate conidia (Klaubauf et al. 2014, Pordel et al. 2017). However, the conidia and conidiophores of *Ps. persiana* are larger than those of *Ps. higginsii*, *Ps. cyperi*, *Ps. kyllingae* and *Ps. hagahagae.* It differs from *Ps. iraniana* in conidial shape and size. To clarify the identification of *Ps. persiana* within *Pseudopyricularia*, *CAL*/ITS/*RPB1* sequences were combined in a phylogenetic analysis. The phylogenetic tree suggested phylogenetic relatedness of the taxa from Iran to *Pseudopyricularia* with high statistical support (Bayesian Posterior Probability = 100 %, Maximum Likelihood bootstrap support =100 %). Our and previous data identified seven species in *Pseudopyricularia*, which is sister to *Macgarvieomyces*. *Macgarvieomyces* is morphologically well-separated from *Pseudopyricularia* because the former produces chlamydospores, has conidiophores that are mostly unbranched and conidia that are narrowly obclavate, granular and 1-septate. Isolates of *Ps. persiana* clustered sister to *Ps. higginsii*. However, conidia and conidiophores sizes of *Ps. persiana* are distinct from those of *Ps. higginsii*. Maximum likelihood and Bayesian Inference analyses of the combined *CAL*, ITS and *RPB1* sequences support the classification of the new species in *Pseudopyricularia*, a genus that is distantly related to *Pyricularia*. Morphological characteristics combined with analyses of DNA sequences allowed us to identify and illustrate *Ps. persiana* as a novel species from Iran.



Maximum Likelihood tree inferred with MEGA v. 6 software (Tamura et al. 2013) from the combined *CAL*, ITS and *RPB1* gene regions of 36 isolates (including GenBank downloaded sequences of 33 taxa from NCBI and newly generated sequences of three taxa from holotype and ex-type). The novel species is shown in **bold**. Bootstrap support values from ML and Bayesian posterior probabilities analyses ≥ 90 % are provided above internodes.

Colour illustrations. Leaves of *Cyperus* sp.; solitary, erect, unbranched and branched conidiophores, obclavate conidia. Scale bars = 10 µm.

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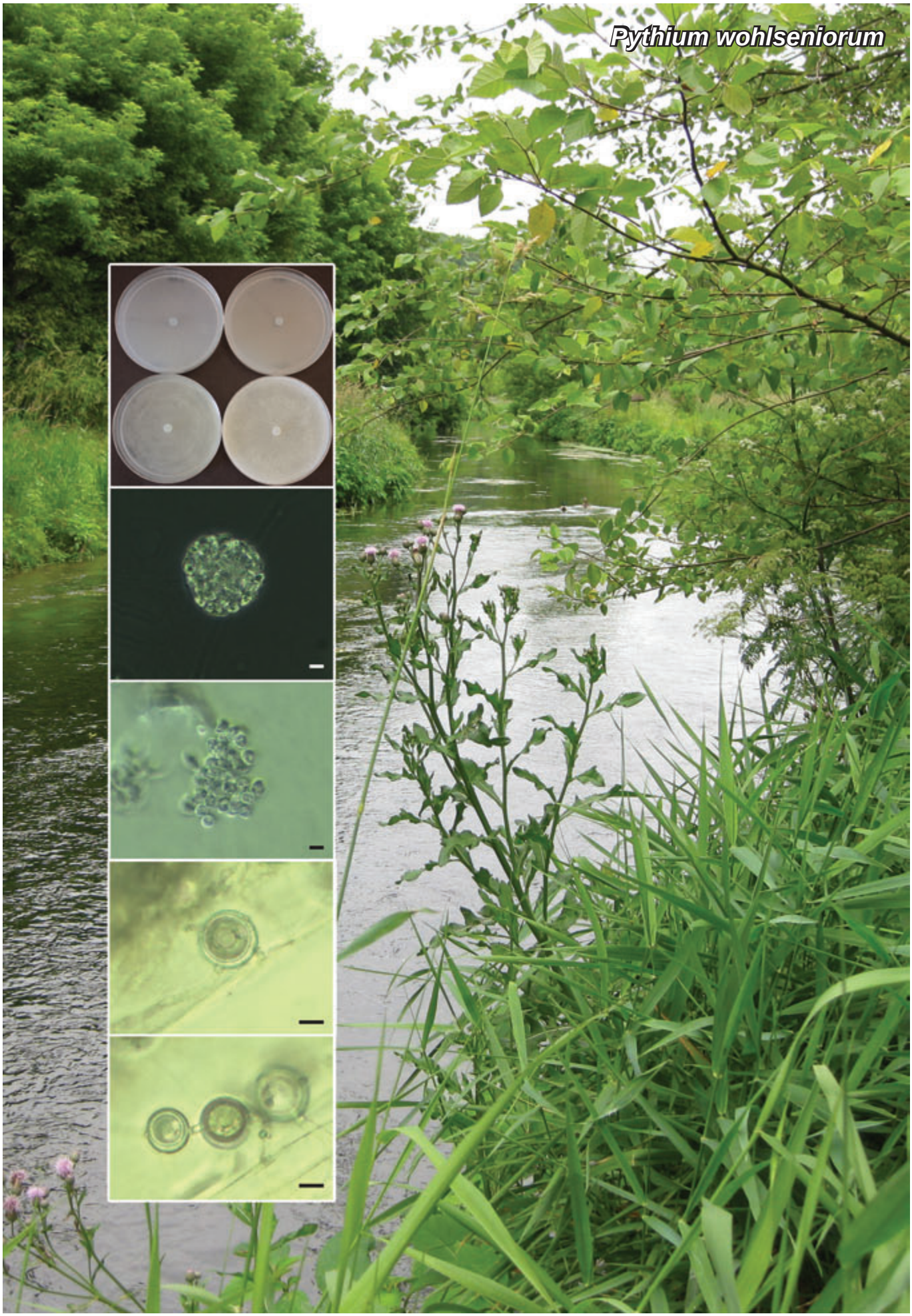

Pythium wohlseniorum

Fungal Planet 861 – 14 December 2018

Pythium wohlseniorum J.E. Blair, *sp. nov.*

Etymology. Named in honour of Carolyn W. and Robert S. Wohlsen, who founded Millport Conservancy in Lititz, Pennsylvania, USA in 1969.

Classification — *Pythiaceae, Pythiales, Oomycetes.*

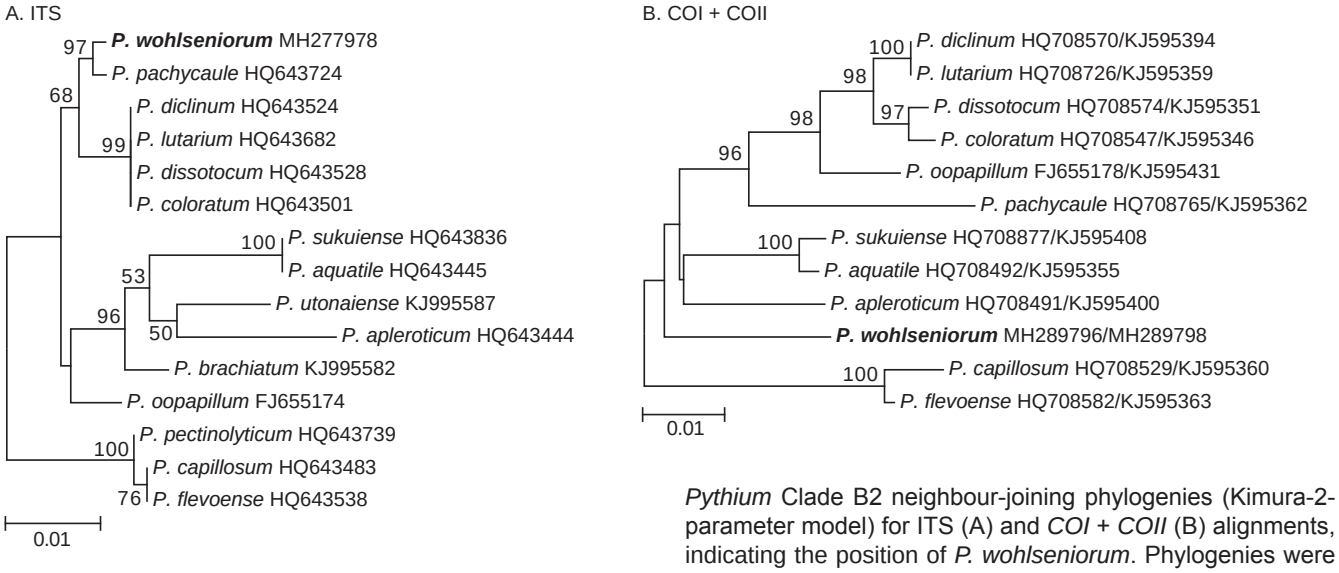
Main *hyphae* up to 5 µm diam. *Sporangia* filamentous non-inflated, giving rise to vesicles containing abundant zoospores at room temperature on 0.2 % water agar with sterile grass blades. *Encysted zoospores* 7–10 µm (av. 8.5 µm) diam, form large grape-like clusters. *Oogonia* produced in single culture after several weeks, globose, smooth-walled, mostly intercalary, occasionally catenulate, 20–23 µm (av. 21.6 µm) diam. *Antheridia* monoclinous, one per oogonium. *Oospores* single, aplerotic or nearly plerotic, globose, 16–19 µm (av. 17.9 µm) diam, wall 1.1–1.6 µm (av. 1.3 µm) thick.

Culture characteristics — Produces dense, aerial hyphae on potato-dextrose agar (PDA), thin aerial hyphae with no special pattern on potato-carrot (PCA) and clarified V8 agars (V8A), and a chrysanthemum pattern with light aerial hyphae on cornmeal agar (CMA). Colony diam. after 24 h at 25 °C on PDA 26 mm, PCA 28 mm, V8A 25 mm, CMA 23 mm. Optimal growth at 28 °C.

Typus. USA, Pennsylvania, Warwick Township, Millport Conservancy, from stream water, 12 May 2015, *J.E. Blair & S. Lobdell* W15-2 (holotype CBS 144501, preserved as metabolically inactive culture, ITS, *COI*, *COII*, beta-tubulin and LSU sequences GenBank MH277978, MH289796, MH289798, MH289799 and MH289800; MycoBank MB826753).

Additional material examined. USA, Pennsylvania, Warwick Township, Millport Conservancy, from stream water, 20 June 2017, *J.E. Blair & A.M. Bauer* (CBS 144502 = W17-58; *COI* sequence GenBank MH289797).

Notes — Isolates were first collected in 2013 and subsequently in 2015 and 2017; this species is commonly baited from stream water with hemp seed, or in association with various submerged pondweeds. Despite extensive stream sampling in the area, *Pythium wohlseniorum* has only been recovered to date from Lititz Run at Millport Conservancy. Phylogenetic analysis of both mitochondrial and nuclear loci place *P. wohlseniorum* in *Pythium* Clade B2 sensu Levesque & De Cock (2004), closely related to *P. pachycaule*. Sequences from 11 isolates were identical for *COII*, ITS, LSU and beta-tubulin loci; a single nucleotide polymorphism was present in *COI* sequences. *Pythium wohlseniorum* has a higher optimal temperature compared to *P. pachycaule*, and a faster growth rate at 25 °C than *P. pachycaule*, *P. coloratum*, *P. diclinum*, *P. dissotoum* and *P. lutarium*. Other morphological features overlap with other Clade B2 species.



Pythium Clade B2 neighbour-joining phylogenies (Kimura-2-parameter model) for ITS (A) and *COI* + *COII* (B) alignments, indicating the position of *P. wohlseniorum*. Phylogenies were reconstructed using MEGA6 (Tamura et al. 2013). Bootstrap support values ≥ 50 % (2000 replicates) are shown on each node; NCBI accession numbers are given after each species name.

Colour illustrations. Lititz Run at Millport Conservancy; culture morphology (clockwise from top-left) on V8A, PCA, CMA and PDA, vesicle containing zoospores, cluster of encysted zoospores, intercalary oogonium with single oospore, catenulate oogonia. Scale bars = 10 µm.

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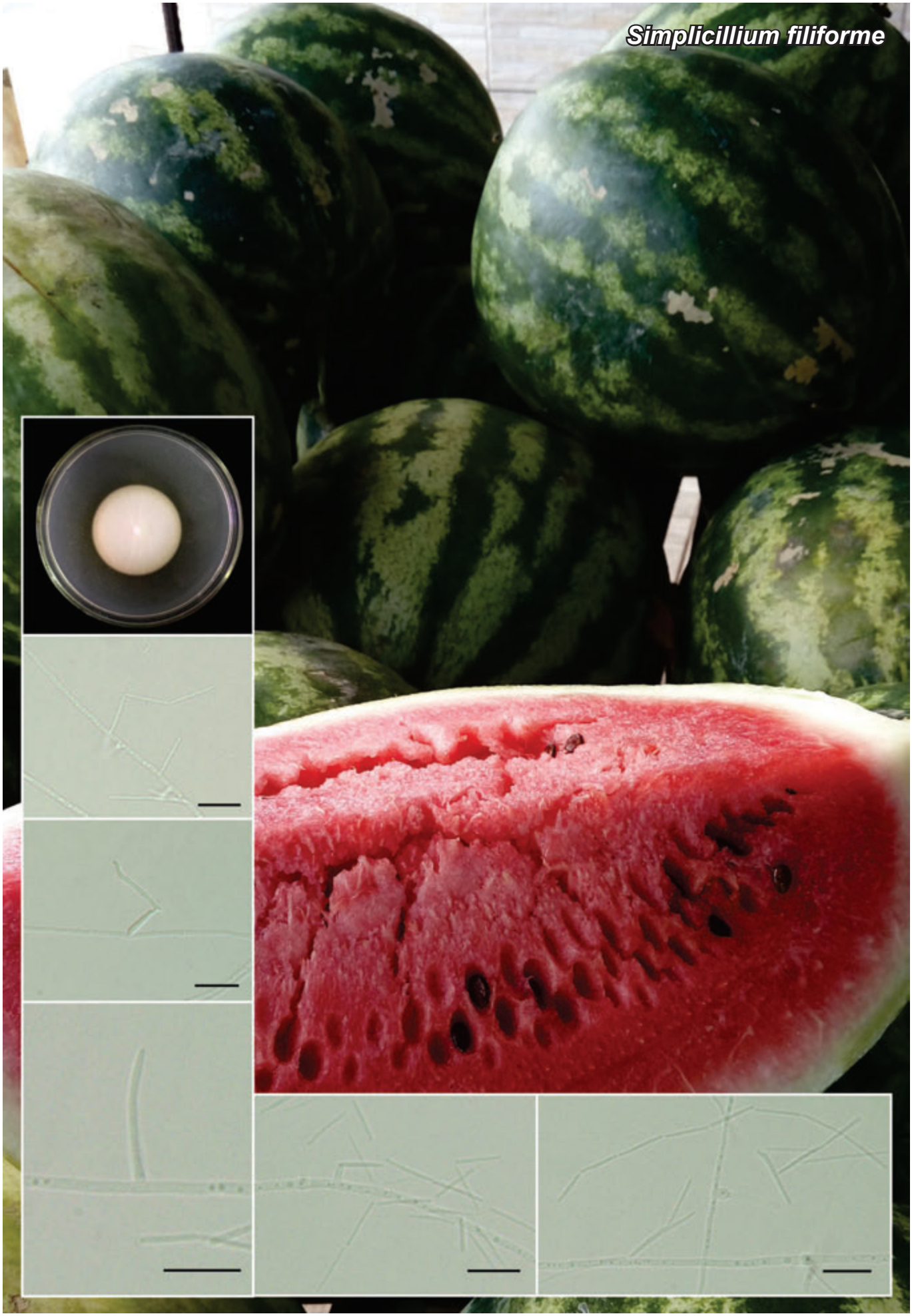

Simplicillium filiforme

Fungal Planet 862 – 14 December 2018

Simplicillium filiforme R.M.F. Silva, R.J.V. Oliveira, Souza-Motta, J.L. Bezerra & G.A. Silva, *sp. nov*.

Etymology. The name refers to the filiform shape of its conidia.

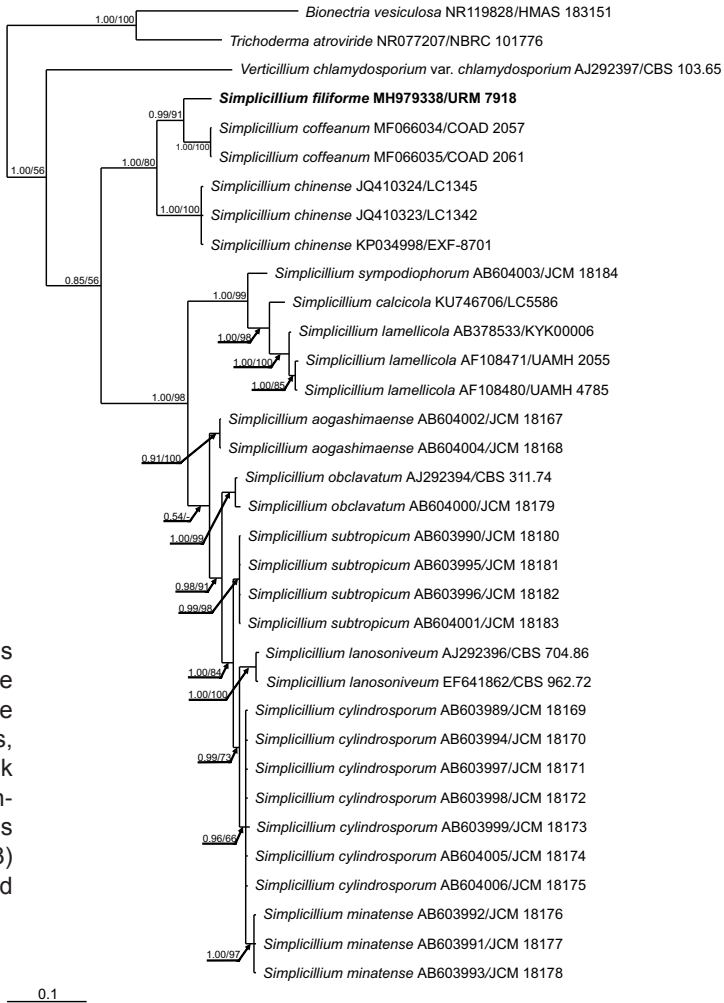
Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelial hyphae thin, hyaline, septate, branched, smooth-walled, 1.8–2.7 µm diam. *Phialides* hyaline, produced on aerial hyphae, solitary, elongate, slightly tapering towards the apex, 9–18 × 1 µm. *Conidia* long, fusoid to filiform, hyaline, smooth-walled, catenulate, straight to curved, sometimes forming zigzag chains, 7.2–12.5 × 1 µm.

Culture characteristics — Colonies on PDA reaching 44 mm diam after 10 d at 25 °C, white, slow growth, moderate aerial mycelium, cottony surface, compact. Reverse white to yellowish cream. Colonies on MEA reaching 40 mm diam after 10 d at 25 °C, white, slow growth, cottony surface, moderate aerial mycelium. Reverse dark yellow.

Typus. Brazil, Pernambuco state, Petrolândia municipality, isolated as endophyte from leaves of *Citrullus lanatus* (*Cucurbitaceae*), 25 July 2016, *R.M.F. Silva* (holotype URM 91886, culture ex-type URM 7918, ITS and LSU sequences GenBank MH979338 and MH979399, MycoBank MB827982).

Notes — The genus *Simplicillium* was introduced by Zare & Gams (2001). Members of this genus include endophytic species, parasites and saprobes isolated from different environments such as soil, freshwater, plants and other parasitic fungi (Liu & Cai 2012, Nonaka et al. 2013, Gomes et al. 2018). Morphologically, *S. filiforme* is similar to *S. obclavatum* and *S. chinense* which also form conidial chains. However, *S. filiforme* is different from *S. obclavatum* and *S. chinense* based on the size and shape of its conidia. *Simplicillium filiforme* produces conidia that are long, fusoid to filiform, catenulate, straight to curved (7.2–12.5 × 1 µm) while *S. obclavatum* produces conidia obclavate to ellipsoidal (2.5–3.5 × 1–2 µm) and *S. chinense* produces conidia that are mostly ovoid, ellipsoidal or cylindrical (3.5–5 × 1–1.5 µm). Based on ITS rDNA, the new species *S. filiforme* is phylogenetically close to *S. coffeanum*, though *S. coffeanum* form macroconidia and microconidia with subglobose to ellipsoidal heads at the apex of the phialides (Gomes et al. 2018).



Bayesian inference (BI) tree obtained by phylogenetic analysis of ITS rDNA sequences from members of *Simplicillium*. The new species is in **bold** face. Support values, shown at the nodes, are from BI and Maximum Likelihood (ML) analyses, respectively. *Bionectria vesiculosa* (HMAS 183151, GenBank NR119828) and *Trichoderma atroviride* (NBRC 101776, GenBank NR077207) were used as outgroup. BI and ML analyses were performed in MrBayes (Ronquist & Huelsenbeck 2003) and PhyML (Guindon & Gascuel 2003), respectively, launched from TOPALi v. 2.5 (Milne et al. 2004).

Colour illustrations. Watermelons for sale, Pernambuco, Brazil; colony on PDA, phialides and conidia, conidial chain. Scale bars = 10 µm.

Rejane M.F. da Silva, Rafael J.V. de Oliveira, Cristina M. Souza-Motta, José L. Bezerra & Gladstone A. da Silva, Departamento de Micologia Prof. Chaves Batista, Universidade Federal de Pernambuco, Recife, Brazil; e-mail: re.biologicas@gmail.com, rafaelvilela87@gmail.com, souzamotta@yahoo.com.br, jlulabezerra@hotmail.com & gladstonesilva@yahoo.com


Superstratomyces tardicrescens

Fungal Planet 863 – 14 December 2018

Superstratomyces tardicrescens Valenz.-Lopez, Rodr.-Andrade, Cano, Guarro & Stchigel, *sp. nov.*

Etymology. From Latin *tarde-*, slowly, and *-crescens*, growing, due to the slow growing rates of the colonies on culture media.

Classification — *Superstratomycetaceae*, *Superstratomycetales*, *Dothideomycetes.*

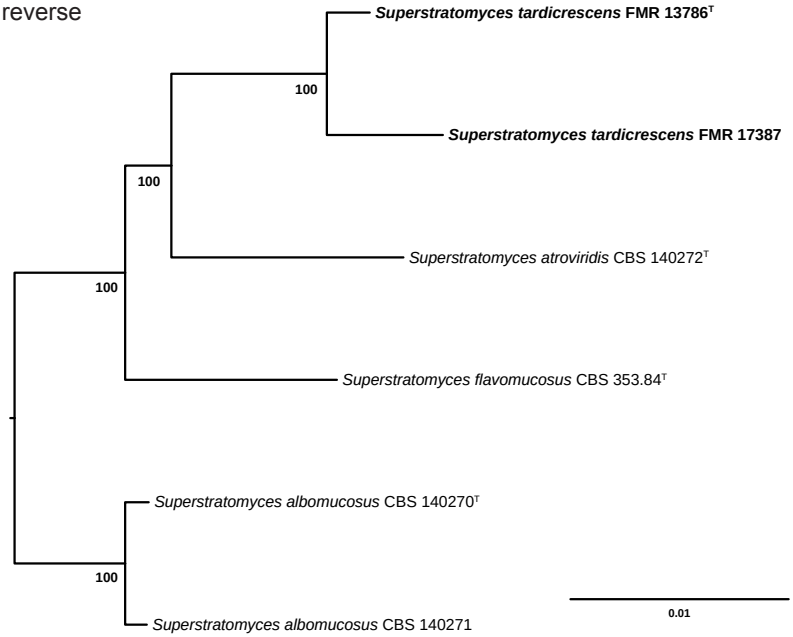
Hyphae hyaline to brown, smooth- and thin- to thick-walled, septate, 2–3.5 mm wide. *Conidiomata* pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, 110–125 mm diam, filled by a white mass of slimy conidia; *pycnidial wall* 25–45 mm broad, pseudoparenchymatous, of *textura angularis*, composed of 3–5 layers of pale brown to brown, flattened polygonal cells of 2.5–5 mm diam. *Setae* erect to recurved, hyaline to subhyaline at apex and turning brown towards the base, 1–2-septate, 10–70 mm in length, 3–5 mm wide at the base, strongly verrucose to tuberculate. *Conidiophores* branched, hyaline, smooth-walled, up to 30–40 µm long, bearing lateral conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, cylindrical to barrel-shaped or ampulliform, 5–8.5 × 1.5–2 µm, smooth-walled, solitary or laterally disposed on the conidiophores. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular, 4–5 × 1.5–2 µm.

Culture characteristics — Colonies on OA reaching 7 mm diam after 14 d at 25 ± 1 °C, margins lobate, flattened, both surface and reverse black (M. 2F1). Colonies on MEA reaching 7 mm diam after 14 d at 25 ± 1 °C, margins lobate, convex, felted, surface white (M. 2A1) to olive grey (M. 2E2); reverse black (M. 2F1).

Typus. USA, South Carolina, from a human eye specimen, 2010, *D.A. Sutton* (holotype FMR H-13786, culture ex-type FMR 13786, ITS, LSU and *tef-1α* sequences GenBank LR025130 and LR025141, MycoBank MB828061).

Additional material examined. Spain, Tarragona, Els Pallaresos, from the darkened surface of a wall house, 19 Apr. 2018, *E. Rodríguez-Andrade*, FMR 17387, ITS, LSU and *tef-1α* sequences GenBank LR025131 and LR025142.

Notes — The geographical origin of the strains (USA and Spain) and the nature of the substrates from which they were isolated (human and environmental ones) probably indicates a wide distribution of this new taxon. *Superstratomyces tardicrescens* is distinguished from the rest of the species of the genus by its small conidia produced on well-developed conidiophores (larger, and produced on single phialides in the rest of the species) (Van Nieuwenhuijzen et al. 2016). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the LSU sequences is *S. atroviridis* CBS 140272 (GenBank NG_058271; Identities = 762/766 (99 %), 1 gaps (0 %)). Closest hits using the ITS sequence is *S. albomucosus* DTO 277-H8 (GenBank KX950421; Identities = 778/790 (98 %), 2 gaps (0 %)). The closest hits using *tef-1α* sequence is *S. flavomucosus* DTO 305-C3 (GenBank KX950470; Identities = 869/889 (98 %), no gaps).



Maximum likelihood tree obtained from the combined DNA sequences dataset from tree loci (ITS, LSU, *tef-1α*) of our isolates and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with T. The new species proposed in this study is indicated in bold. The RAxML bootstrap support values (≥ 70 %) are provided at the nodes. *Superstratomyces albomucosus* was used as outgroup.

Colour illustrations. USA, South Carolina; colony on OA and MEA after 14 d at 25 ± 1 °C; conidiomata under the stereomicroscope; pycnidia, conidiophores, conidiogenous cells and conidia. Scale bars: 50 µm (pycnidia), 10 µm (conidiophores, conidiogenous cells and conidia).

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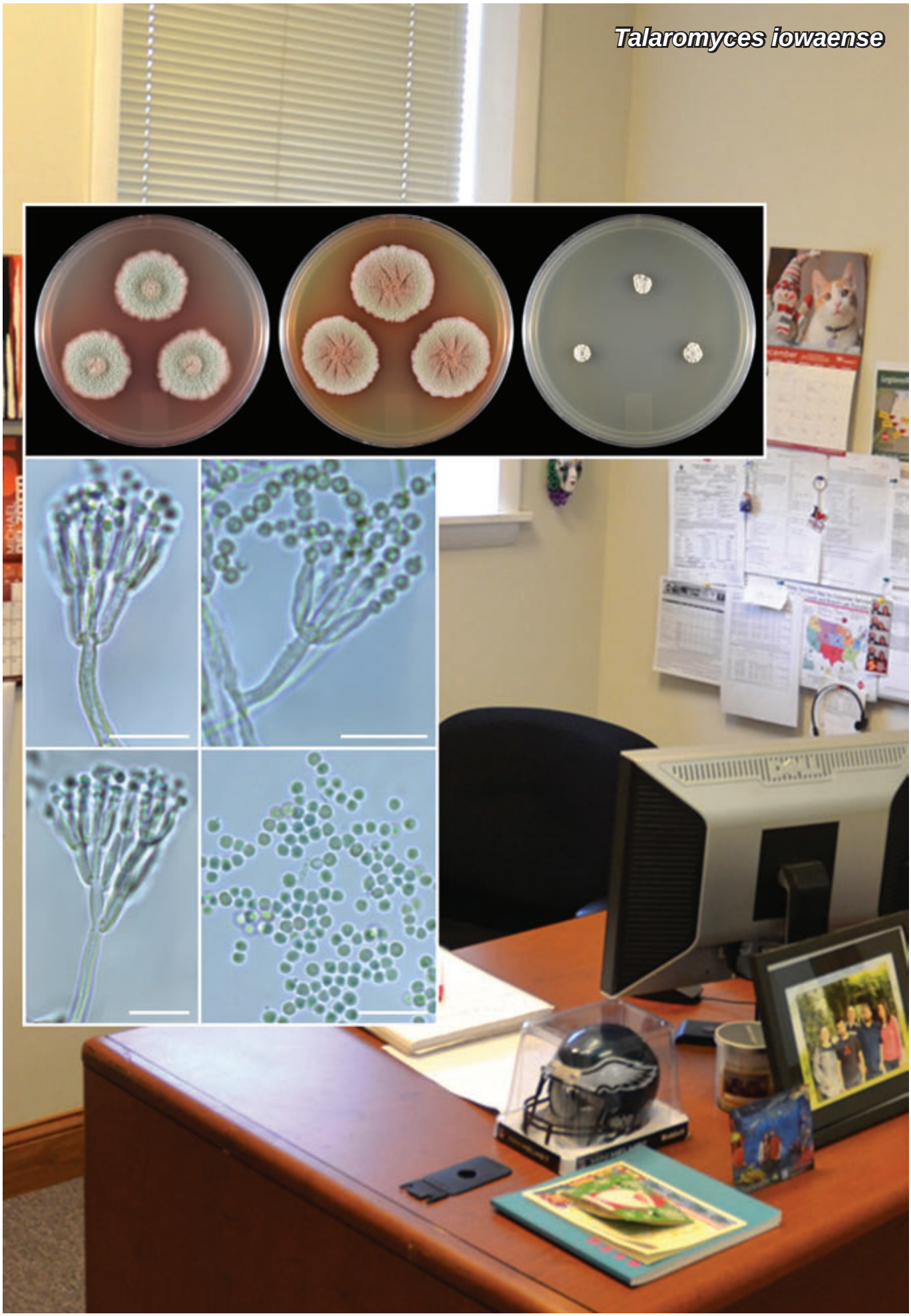
Talaromyces iowaense

Fungal Planet 864 – 14 December 2018

Talaromyces iowaense Jurjević, G. Perrone, S.W. Peterson, A. Susca, F. Epifani, *sp. nov.*

Etymology. Named for Iowa, USA, where the fungal culture was isolated.

Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes.*

On MEA. *Conidiophores* (8–)25–85(–135) × (2–)2.5–3(–4) µm, borne from surface and from aerial rope-like hyphal aggregations, with smooth to finely roughened walls, bearing terminal biverticillate, or more complex, occasionally monoverticillate penicilli, metulae (5–)6–10(–16) × 2–4 µm, smooth to finely roughened, in verticils of (2–)4–9(–11), phialides acerose, (6–)7–9(–11) × 2–3 µm, with long, gradually tapering collula, smooth to occasionally finely roughened, (2–)5–7(–9) per metula. *Conidia* sub-spherical to spherical, 2–2.5(–3) × 2–3 µm, with finely roughened walls, borne in short disordered chains. No *sexual morph* observed.

Culture characteristics — (in darkness, 25 °C after 14 d): Colonies on malt extract agar (MEA) 30–31 mm diam, colony texture floccose to funiculose, centrally rising c. 3 mm, occasional shallow radial sulci, mycelium white to pink (Venetian pink R13; Ridgway 1912) or reddish orange (orange rufous, R2), sporulation heavy, conidia *en masse*, light celandine green to Artemisia green (R47), exudate absent, soluble pigments red (light coral red to Pompeian red, R8), reverse mahogany red (R2) to light pinkish cinnamon (R29). Colonies on Czapek yeast autolysate agar (CYA) 3–4 mm diam, mycelium white, subsurface or submerged hyphae, sporulation not observed, exudate absent, soluble pigments absent, reverse cartridge buff to cream-buff (R30). Colonies on potato dextrose agar (PDA) 25–26 mm diam, colony texture floccose to funiculose, moderate deep to deep radial sulci, mycelium white to deep vinaceous (R27), sporulation moderate to heavy, in zones, conidia *en masse* pale green-blue grey to deep green-blue grey blue (R48), exudate clear, soluble pigments absent, reverse orange-vinaceous (R27) to orange-cinnamon (R29) to cream-buff (R30), marginally. Colonies on Czapek yeast agar with 20 % sucrose (CY20S) 2–3 mm diam, colony texture floccose to funiculose, mycelium white to ochraceous-orange (R15), sporulation moderate to very good, conidia *en masse* pale greenish blue grey to deep greenish blue grey (R48), pale green-blue grey to deep green-blue grey (R48), exudate absent, soluble pigments absent. Colonies on dichloran-glycerol agar (DG18) 11–12 mm diam, colony texture funiculose, at margins 2–3 mm diam subsurface to submerged hyphae, mycelium white, sporulation moderate, conidia *en masse* not coloured, exudate absent, soluble pigments absent, reverse cartridge buff to cream-buff (R30). No growth on CYA with 5 % NaCl (CYAS). Colonies on oatmeal agar (OA) 9–10 mm diam, colony texture floccose to funiculose, abruptly rising c. 4–5 mm, mycelium white, inconspicuous, heavy sporulation, conidia *en masse* glaucous-grey to deep greyish blue-green (R48), exudate absent, soluble pigments absent. Colonies on creatine sucrose agar (CREA), up to 8 mm diam, no acid production. Colony diam, 14 d (mm): CYA/MEA 20 °C 2–3/22–24; 30 °C 3–4/33–35; 35 °C 1–2/9–11; no growth at 37 °C. Colony diam, 7 d (mm): CYA 1–2; MEA 17–18; PDA 10–12; CY20S no growth to germinate; DG18 3–4; CYAS no growth; OA 6–7 mm; CREA up to 4 mm; Colony diam, 7 d (mm): CYA/MEA 20 °C germinate/12–13; 30 °C 1–2/19–20; 35 °C germinate/5–6; no growth at 37 °C.

Typus. USA, Iowa, Jefferson, office, air, 27 Jan. 2014, *Ž. Jurjević* (holotype BPI 910643, cultures ex-type NRRL 66822 = ITEM 17527 = EMSL 2233, ITS, *BenA*, *CaM* and *rpb2* sequences GenBank MH281565, MH282578, MH282579 and MH282577, MycoBank MB828092).

Notes — BLAST searches of the sequences of *Talaromyces iowaense* showed β-tubulin (*BenA*) similarity to *T. rademirici* (83 %), calmodulin (*CaM*) similarity to *T. purpureus* (82 %), RNA polymerase II second largest subunit (*rpb2*) similarities to *T. rademirici* (89 %) and *T. purpureus* (87 %), and ITS similarity to *T. purpureus* was 91 %.

A phylogenetic tree with three genes was generated (no *T. rademirici* calmodulin sequence available), and the branch resolution improved when this species is included. The maximum likelihood analysis of DNA sequences show net separation of this new species from the other well-resolved branches. *Talaromyces iowaensis* clusters with the species from *Talaromyces* sect. *Purpurei. Talaromyces iowaense* is distinguished from other *Talaromyces* species by production of intense red (light coral red to Pompeian red, R8) soluble pigments on MEA, good growth on MEA but restricted on CYA, growth on CREA, no growth at 37 °C, and conidia 2–2.5(–3) × 2–3 µm. The closely related *T. rademirici* demonstrates no soluble pigments on MEA, good growth on CYA and MEA, no growth on CREA, growth at 37 °C, and has larger conidia 2.5–4 × 1.5–2.5 µm.

For supplementary information see MycoBank.

Colour illustrations. Air, office; 14-d-old cultures of *Talaromyces iowaense* on MEA (left: 25 °C, middle: 30 °C, right: 35 °C), conidia and conidiophores on MEA. Scale bars = 10 µm.

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Thozetella pindobacuensis

Fungal Planet 865 – 14 December 2018

Thozetella pindobacuensis T.A.B. Santos, L.B. Conç. & Gusmão, *sp. nov.*

Etymology. Referring to the municipality of Pindobaçu where this fungus was collected.

Classification — *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetes.*

Colonies on natural substrata effuse, whitish. *Mycelium* partly superficial, partly immersed in the substrata, hyphae septate, branched, cylindrical cells, 1.5–2.5 µm diam, smooth-walled, pale brown. *Stromata* absent. *Conidiomata* synnematal, infundibuliform, campanulate, convex and wide at the apex, straight, unbranched, brown, pale brown to pale yellowish brown, 154–200 µm high, 30–65.5 µm wide at the base, 255–311 µm wide at the apex, with synchronous extensions. *Conidiophores* macronematous, septate, cylindrical, smooth, pale brown. *Conidiogenous cells* monophialidic, integrated, determinate, terminal, cylindrical, smooth, pale brown, 10–21 × 1.5–2.5 µm, collarette absent. *Conidia* lunate, fusiform, ellipsoid-fusoid, rarely naviculate, continuous, guttulate or eguttulate, hyaline, 13.5–18 × 1.5–2 µm, provided with a single setula at each end, setulae 4.5–7 µm long. *Microawns* awn-like, L-shaped to almost straight, 0–1-septate, smooth, refractive, hyaline, 19–75 × 1.5–3.5 µm, basal part thin-walled.

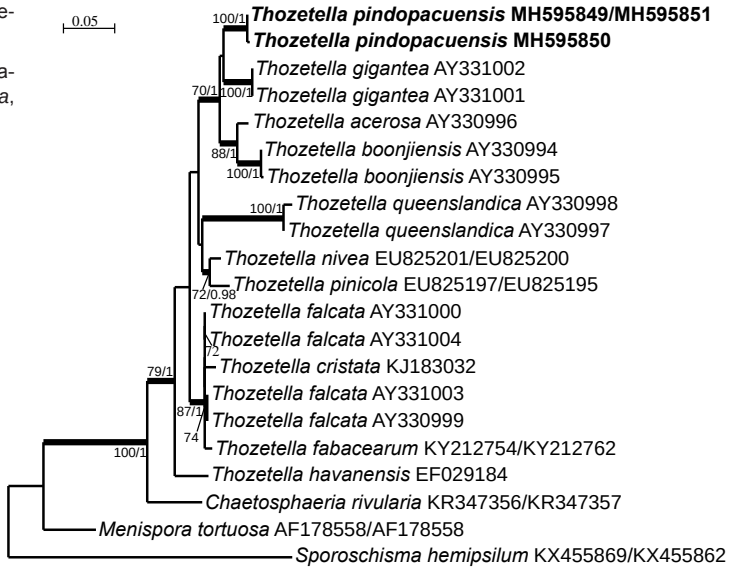
Culture characteristics — Colonies on 2 % malt extract agar (MEA), reaching 55 mm diam after 15 d at 25 °C, immersed mycelium, semicircular, entire edges, whitish. Reproductive structures and microawns present on the surface of the culture medium and abundant in the centre and the edge of the colony.

Typus. Brazil, Bahia, Pindobaçu, Serra da Fumaça, on decaying leaves of unidentified plant, 19 Feb. 2017, *L.B. Conceição* (holotype HUEFS239376, isotype HUEFS239377, cultures ex-type LAMIC0122/17, ITS and LSU sequences GenBank MH595849 and MH595851, MycoBank MB827077).

Additional specimen examined. Brazil, Ceará, Ubajara, Serra de Ibiapaba, on decaying leaves of *Vismia guianensis*, 5 July 2012, *L.A. Costa*, LAMIC0134/12, ITS sequence GenBank MH595850.

Colour illustrations. Background photo of Serra da Fumaça; 15-d-old culture on MEA, conidiomata with synchronous extensions, conidiogenous cells, conidia and microawns. Scale bars = 20 µm.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *T. gigantea* (GenBank AY331002 and AY331001; Identities = 432/442 and 431/442 (98 %), no and 1 gap, respectively), *T. acerosa* (GenBank AY330996; Identities = 440/455 (97 %), 1 gap) and *T. boonjiensis* (GenBank AY330995; Identities = 424/442 (96 %), 1 gap). Closest hits using the LSU sequence had highest similarity to *T. fabacearum* (GenBank NG_059767 and KY212762; Identities = 499/518 (96 %), 6 gaps (1 %)), *T. nivea* (GenBankEU825200; Identities = 497/518 (96 %), 6 gaps (1 %)) and *Chaetosphaeria rivularia* (GenBankKR347357; Identities = 490/519 (94 %), 7 gaps (1 %)). Morphologically, *T. pindobacuensis* differs from *T. gigantea* based on the size of the microawns (65–280 × 2.5–8 µm) and conidial setula (6–12.5 µm long) (Paulus et al. 2004, Silva & Grandi 2013). Furthermore, the new species has synnematous conidiomata with synchronic extensions and 0–1-septate microawns. *Thozetella pindobacuensis* differs from *T. acerosa*, *T. boonjiensis* and *T. nivea* in the production of sporodochial conidiomata and the shape of its microawns. In this paper, we considered *T. acerosa* and *T. boonjiensis* as distinct species based on molecular data (Paulus et al. 2004, Jeewon et al. 2009, Perera et al. 2016).



Maximum likelihood (ML) tree based on combined dataset of ITS and LSU sequences. The ML analysis was performed using RAxML v. 8.2.10. The Bayesian inference (MrBayes v. 3.2.6) was performed under a GTR+G+I model for 2 M generations. The values of ML bootstrap (BP-ML) and posterior probabilities (PP-BI) were plotted at the nodes for which threshold values (BP-MP: > 50 % / BP-ML: > 70 % / PP: > 0.95) were achieved. One access number = ITS; two access numbers ITS and LSU sequences, respectively. The novel species is indicated in **bold** face.

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Xenosonderhenia coussapoae

Fungal Planet 866 – 14 December 2018

Xenosonderhenia coussapoae J.L. Alves & R.W. Barreto, *sp. nov.*

Etymology. Name reflects the host genus from which it was isolated, *Coussapoa*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Leaf spots amphigenous, irregular, 1–7 mm diam, medium brown with irregular edges, white patches due to raised epidermis, surrounded by a wide, red-purple border and with abundant fungal structures abaxially. *Internal mycelium* indistinct. *External mycelium* superficial, up to 2–3 µm diam, branched, septate, pale brown, smooth. *Stromata* absent. *Conidiophores* arising from external mycelium, either isolated or clustering on trichomes, cylindrical, 17.5–40 × 5–7.5 µm, 1–3-septate, not branched, hyaline to subhyaline, smooth. *Conidiogenous cells* terminal or intercalary, subcylindrical, 18–39.5 × 5–7 µm, smooth. *Conidiogenous loci* protuberant, 3–7 per cell up to 1 µm diam, not thickened nor darkened. *Conidia* cylindrical, straight, 10–29 × 1–4 µm, 1–3-septate, base truncate, 1–2 µm diam, apex rounded, hyaline to subhyaline, smooth.

Culture characteristics (under 12 h light regime, at 25 °C) — Slow growing (12–15 mm diam after 12 d), aerial mycelium sparse, lobate margins, white to buff with some overlapping areas smoke grey, reverse pale luteus to honey. Cultures sterile.

Typus. Brazil, Viçosa, campus of Universidade Federal de Viçosa, on *Coussapoa floccosa* (*Cecropiaceae*), 18 July 2014, *R.W. Barreto* (holotype VIC44404, culture ex-type COAD1824; ITS and LSU sequences GenBank MG780415 and MH716814, MycoBank MB827438).

Notes — *Xenosonderhenia* was recently established to accommodate two leaf spot fungal pathogens belonging to the *Mycosphaerellaceae*. *Xenosonderhenia* is a pleomorphic genus including the type species *X. syzygii* – with no known sexual morph but described as having two asexual morphs: a pycnidial morph and a hyphomycete synasexual morph seen only in culture (Crous et al. 2012b) and *X. eucalypti* – known only from its ascomatal morph (Crous et al. 2014b). Phylogenetically, COAD1824 clusters with *Mycosphaerella elaeocarpi* – a fungus lacking an asexual morph – and with *Xenosonderhenia.* Morphological features such as size and surface of conidia (finely verruculose in *X. syzygii* but smooth in the newly proposed species) and phylogenetic data indicated that the fungus on *C. floccosa* represents a new species of *Xenosonderhenia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence were *X. syzygii* (GenBank NR_111763; Identities = 461/492 (94 %), 7 gaps (1 %)), *X. eucalypti* (GenBank NR_137937; Identities = 457/492 (93 %), 6 gaps (1 %)) and *Mycosphaerella elongata* (GenBank EF394833; Identities = 456/492 (93 %), 8 gaps (1 %)). Closest hits for LSU were *M. elaeocarpi* (GenBank EU040212; Identities = 858/868 (99 %), 4 gaps (0 %)), *X. syzygii* (GenBank NG_042685; Identities = 852/864 (99 %), 2 gaps (0 %)) and *X. eucalypti* (GenBank NG_058120; Identities = 812/823 (99 %), no gaps).

Xenosonderhenia coussapoae represents an addition to the known mycobiota of *C. floccosa* and, if proven specific to this host, may represent an endangered species of microfungi, as are other fungal species described from this highly endangered Brazilian tree species (Rocha et al. 2010).

Colour illustrations. Leaf spots on *Coussapoa floccosa*; leaf spot, conidiophores and conidia on trichomes (SEM). Scale bars = 20, 20, 5, 40 and 20 µm, respectively.

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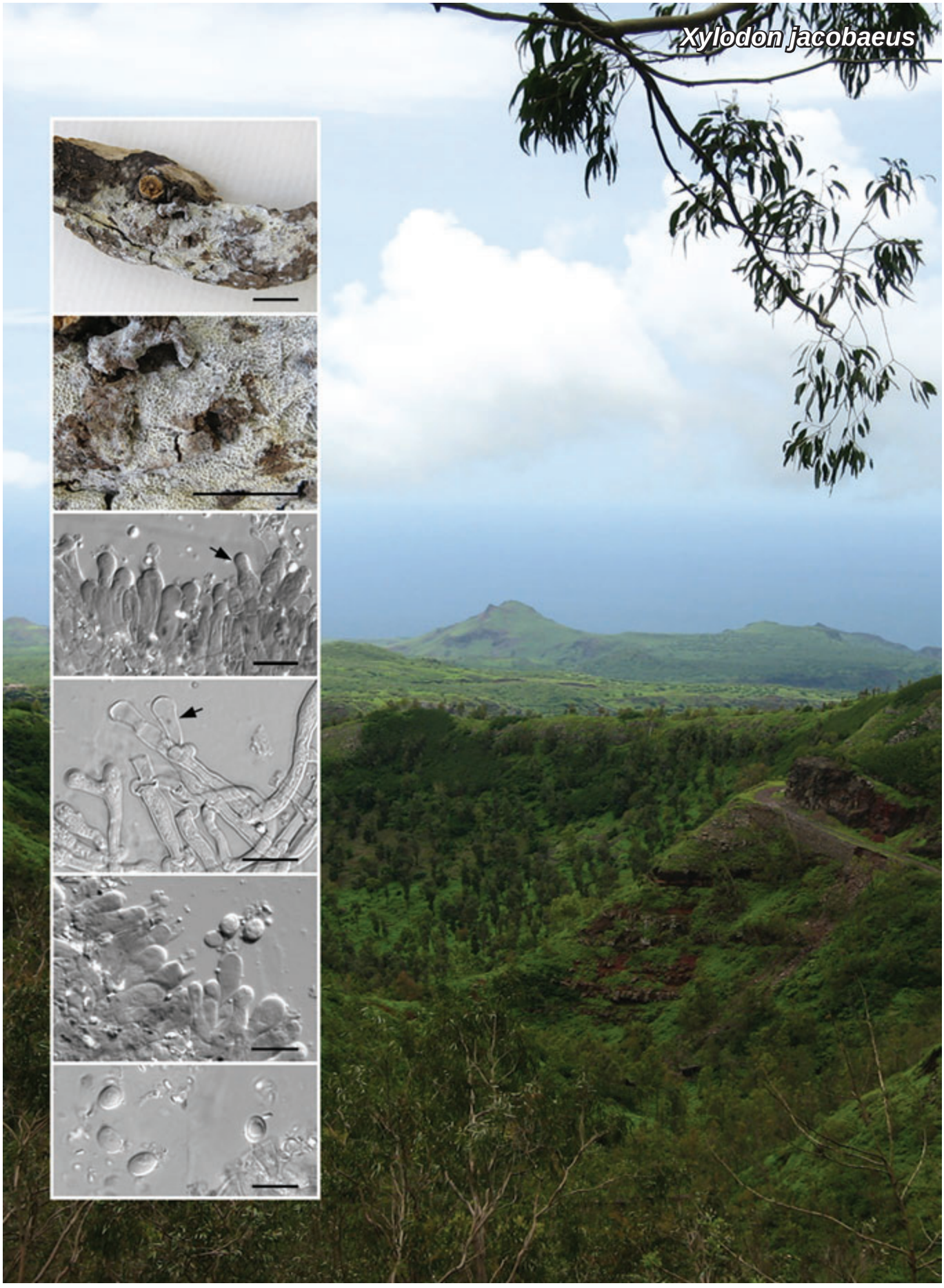
Xylodon jacobaeus

Fungal Planet 867 – 14 December 2018

Xylodon jacobaeus J. Fernández-López, M. Dueñas, M.P. Martín & Telleria, *sp. nov.*

Etymology. Named after Santi Jacobi Insula, Latin name for Santiago Island, Cape Verde Archipelago, where it was collected.

Classification — *Schizoporaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma resupinate, effuse, adnate; hymenophore reticulate to poroid, 1–2 pores/mm, yellowish white to pale yellow (92. y White – 89. p. Y; Kelly & Judd 1976) margin not clearly differentiated, sometimes paler. *Hyphal system* monomitic; hyphae hyaline, thin to slightly thickened walls, sparsely branched, with clamps, 2.5–3.5 µm wide; subicular hyphae loosely interwoven, parallel to substratum; subhymenial hyphae more densely interwoven, perpendicular to substratum, usually slightly encrusted. *Cystidia* or rather cystidial elements present: 1) capitate cystidia arise from the hymenium, subcylindrical to utriform, thin-walled, basal clamped, 20–24 × 4–7 µm; and 2) capitate hyphae arise from the subiculum, basal clamped, 15–35 × 2.5–3.5 µm, apex up to 7 µm diam. *Basidia* claviform to subclaviform, sometimes pedunculated, 17–20 × 4–5 µm, internal linear repetition seems to occur occasionally, four sterigmata, with basal clamp. *Spores* ellipsoid, (5–)6–7 × (3.5–)4–4.5 µm, hyaline, thin-walled, smooth, guttulate, L = 6.24, W = 4.35, Q = 1.43 (n = 32/3).

Habitat & Distribution — On debris of *Eucalyptus camaldulensis* and *Lantana camara*; known from two localities of Santiago Island, Cape Verde Archipelago.

Typus. Cape Verde, Santiago island, São Domingos, Rui Vaz, N15°01'59" W23°37'06", 873 msl, on *Eucalyptus camaldulensis* (*Myrtaceae*), 21 Sept. 2010, *J. Cardoso*, *L.M. Catarino*, *M. Dueñas*, *M.P. Martín*, *I. Melo*, *I. Salcedo & M.T. Telleria*, 18975Tell. (holotype MA-Fungi 91340, ITS sequence GenBank MH430073, MycoBank MB826918).

Additional specimens examined. Cape Verde, Santiago island, Santa Catarina, Serra da Malagueta Natural Park, N15°10'41.5" W23°41'14.2", 907 msl, on *Lantana camara*, 20 Sept. 2010, *J. Cardoso*, *L.M. Catarino*, *M. Dueñas*, *M.P. Martín*, *I. Melo*, *I. Salcedo & M.T. Telleria*, 13224MD, MA-Fungi 91338, ITS sequence GenBank MH430074; ibid., 13225MD, MA-Fungi 91339, ITS and LSU sequences GenBank MH430072 and MH430071).

Notes — Maximum likelihood phylogenetic analyses of ITS sequences under a GTR model grouped the new sequences in a well-supported clade (bootstrap support value > 95 %) with *Xylodon niemelaei*, *X. rhizomorphus* and *X. reticulatus*. No LSU GenBank sequences were available for *X. reticulatus*. Distribution and morphological diagnostic characters for each species are shown in Table 1. *Xylodon jacobaeus* is similar to these species, but differs in having subcylindrical to utriform cystidia, capitate hyphae and wider spores.

Topology of ITS tree obtained by Maximum Likelihood Inference conducted in RAxML v. 8.2.10 on CIPRES Science Gateway v. 3.3 (Miller et al. 2010). Two sequences of *X. paradoxus* were used as outgroup. Bootstrap support values (> 50 %) are indicated on the branches (bootstrap iterations = 1 000). The *X. jacobaeus* clade is marked with a green block; the accession numbers from the EMBL/GenBank database are indicated at the terminal nodes. The asterisk (*) after the EMBL/GenBank accession numbers are sequences obtained for this study.

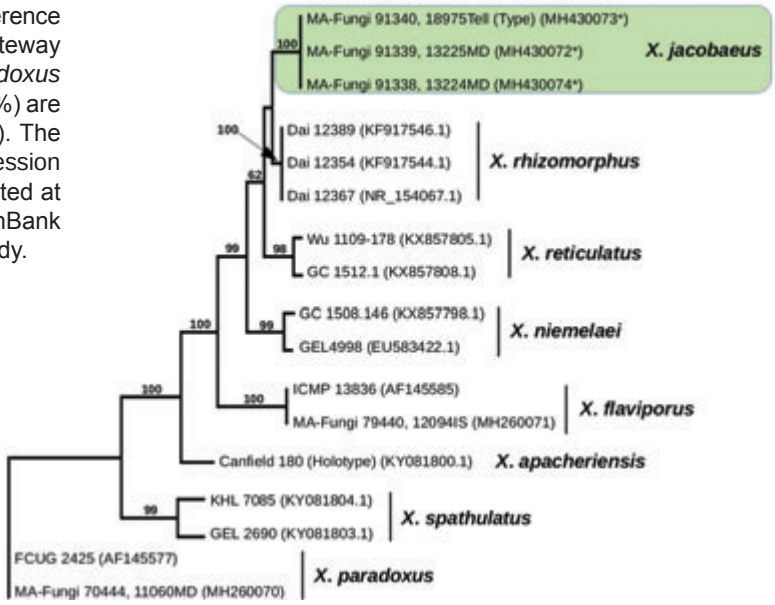

Table 1 Comparison of distribution and micromorphology of *Xylodon jacobaeus* and closely related species.

Species	Type locality	Cystidia and cystidial elements	Spores	References
X. niemelaei	Taiwan	Capitate and subulate cystidia	5–5.5(–6) × 3.5–4 µm	Wu (1990)
X. rhizomorphus	China	Bladder-like cystidia	(4.1–)4.3–5.5(–5.9) × (3.5–)3.7–4.1(–4.3) µm	Zhao et al. (2014)
X. reticulatus	Taiwan	Capitate, subclavate to clavate and slightly moniliform cystidia; short encrusted hyphal apices	(4.8–)5–6(–7) × 3–3.6(–4) µm	Chen et al. (2017)
X. jacobaeus	Cape Verde	Capitate, subcylindrical to utriform cystidia; capitate hyphae	(5–)6–7 × (3.5–)4–4.5 µm	Present study

Colour illustrations. Cape Verde, Santiago, São Domingos, Rui Vaz (photo credit M.T. Telleria); From top to bottom: basidioma (MA-Fungi 91340), cystidia, capitate hyphae, basidia and spores (MA-Fungi 91340). Scale bars = 1 cm (basidioma), 10 µm (all others).

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